

OM protein - protein search, using sw model

Run on: March 9, 2005, 01:48:13 ; Search time 89.8081 Seconds
(without alignments)
370.361 Million cell updates/sec

Title: US-10-054-873-4
Perfect score: 463
Sequence: 1 FVNQHLCGSHLVEALYLVCG.....IVEQCCTSICSLYQLENYCN 86

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	463	100.0	86	1	AAP40829	Aap40829 Sequence
2	463	100.0	86	2	AAR84061	Aar84061 Human ins
3	463	100.0	86	2	AAY42858	Aay42858 Human ins
4	463	100.0	86	3	AAB12770	Aab12770 Human pro
5	463	100.0	86	5	AAM48218	Aam48218 Human pro
6	463	100.0	86	7	ADC64463	Adc64463 Amino aci
7	463	100.0	86	7	ADF16632	Adf16632 Human alb
8	463	100.0	86	7	ADH21860	Adh21860 Human lon
9	463	100.0	86	8	ADT93277	Adt93277 Human nat

10	463	100.0	87	1	AAP20036	Aap20036	Human pro
11	463	100.0	87	1	AAP40217	Aap40217	Sequence
12	463	100.0	87	1	AAP50127	Aap50127	Sequence
13	463	100.0	87	1	AAP50060	Aap50060	Synthetic
14	463	100.0	87	1	AAP61090	Aap61090	Sequence
15	463	100.0	87	2	AAR32367	Aar32367	Proinsuli
16	463	100.0	88	2	AAR07682	Aar07682	Modified
17	463	100.0	88	2	AAR33855	Aar33855	hpI. 3/20
18	463	100.0	92	2	AAR20467	Aar20467	Yeast alp
19	463	100.0	92	8	ADL24442	Adl24442	Modified
20	463	100.0	93	1	AAP90102	Aap90102	Synthetic
21	463	100.0	96	2	AAAY08004	Aay08004	Human pro
22	463	100.0	96	2	AAO17830	Aao17830	Human pro
23	463	100.0	96	8	ADL24437	Adl24437	Modified
24	463	100.0	97	2	AAR68898	Aar68898	Human pro
25	463	100.0	97	3	AAB12773	Aab12773	Human pro
26	463	100.0	110	1	AAP10042	Aap10042	Sequence
27	463	100.0	110	1	AAP10053	Aap10053	Sequence
28	463	100.0	110	1	AAP40309	Aap40309	Sequence
29	463	100.0	110	2	AAAY06608	Aay06608	Human pre
30	463	100.0	110	2	ADF77582	Adf77582	Human ins
31	463	100.0	110	3	AAAY44367	Aay44367	Human pro
32	463	100.0	110	3	AAAY70366	Aay70366	Human Ins
33	463	100.0	110	3	AAB26765	Aab26765	Human pre
34	463	100.0	110	3	AAB06144	Aab06144	Human ins
35	463	100.0	110	4	AAE10337	Aae10337	Human pre
36	463	100.0	110	4	AAB35424	Aab35424	Secretory
37	463	100.0	110	4	AAG65677	Aag65677	Human pro
38	463	100.0	110	5	ABG60634	Abg60634	Human ins
39	463	100.0	110	5	ABG31590	Abg31590	Human pre
40	463	100.0	110	6	ABR55862	Abr55862	Humanised
41	463	100.0	110	6	ADA09218	Ada09218	Human Pre
42	463	100.0	110	7	ADC51569	Adc51569	Human pro
43	463	100.0	110	7	ADE56710	Ade56710	Human Pro
44	463	100.0	110	7	ADD46938	Add46938	Human Pro
45	463	100.0	110	7	ADE57650	Ade57650	Human Pro

ALIGNMENTS

RESULT 1

AAP40829

ID AAP40829 standard; protein; 86 AA.

XX

AC AAP40829;

XX

DT 09-SEP-2004 (revised)

DT 25-MAR-2003 (revised)

DT 03-AUG-1992 (first entry)

XX

DE Sequence of human insulin precursor.

XX

KW Insulin precursor; connecting peptide; diabetes; hormone.

XX

OS Homo sapiens.

OS Unidentified.

XX
 FH Key Location/Qualifiers
 FT Region 1. .30
 FT /label= chain B
 FT Modified-site 1
 FT /label= F-NH2-R
 FT /note= "H or a chemically or enzymatically cleavable AA
 FT residue or peptide residue"
 FT Disulfide-bond 7. .72
 FT Disulfide-bond 19. .85
 FT Peptide 31. .65
 FT /label= connecting peptide
 FT Region 66. .86
 FT /label= chain A
 FT Disulfide-bond 71. .76
 FT Modified-site 86
 FT /label= N-OH
 XX
 PN US4430266-A.
 XX
 PD 07-FEB-1984.
 XX
 PF 16-FEB-1982; 82US-00349397.
 XX
 PR 27-MAR-1980; 80US-00134389.
 PR 28-NOV-1980; 80US-00210696.
 XX
 PA (ELIL) LILLY & CO ELI.
 XX
 PI Frank BH;
 XX
 DR WPI; 1984-049032/08.
 XX
 PT Insulin precursor prodn. from linear S-sulphonate and mercaptan - in
 PT single step without separate oxidn.
 XX
 PS Claim 17; Col 4; 8pp; English.
 XX
 CC The inventors claim a method for the prepn. of an insulin precursor in
 CC which the A-chain and B-chain are joined through a connecting peptide.
 CC The connecting peptide joins the A-chain at the amino group of A-1 to the
 CC B-chain at the carboxyl group of B-30. The method is pref. for the prepn.
 CC of human insulin precursor (see AAP40829). The SQs of the connecting
 CC peptides of a number of species are given (see AAP40828, AAP40830-39).
 CC (Updated on 25-MAR-2003 to correct PA field.)
 CC
 CC Revised record issued on 09-SEP-2004 : Correction to Feature Table Key
 XX
 SQ Sequence 86 AA;

Query Match 100.0%; Score 463; DB 1; Length 86;
 Best Local Similarity 100.0%; Pred. No. 1.5e-43;
 Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60

Qy . 61 SLQKRGIVEQCCTSICSLYQLENYCN 86
|||||
Db 61 SLQKRGIVEQCCTSICSLYQLENYCN 86

RESULT 2

AAR84061

ID AAR84061 standard; protein; 86 AA.

XX

AC AAR84061;

XX

DT 22-AUG-1996 (first entry)

XX

DE Human insulin.

XX

KW Insulin; transformation; gene expression; fungi; fungal cell; hormone;

KW A-chain; C-chain; glycosylation.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 1. .261

FT /*tag= a

FT /product= "Insulin."

XX

PN EP704527-A2.

XX

PD 03-APR-1996.

XX

PF 03-AUG-1995; 95EP-00112210.

XX

PR 05-AUG-1994; 94HR-00000432.

XX

PA (PLIV) PLIVA PHARM & CHEM FAB.

XX

PI Mestric S, Punt PJ, Valinger R, Van Den Hondel CAMJJ;

XX

DR WPI; 1996-129917/18.

DR N-PSDB; AAT17830, AAT17831.

XX

PT DNA encoding human insulin precursors - which comprise B- and A-chains

PT linked via amino acid chain contg. 1 or more glycosylation sites, for

PT prepn. of insulin in fungal cells.

XX

PS Disclosure; Fig 1; 32pp; English.

XX

CC DNA sequences encoding insulin precursors of formula B-Pg-A, where B and

CC A represent B- and A-chains of insulin respectively, and Pg represents a

CC modified C-peptide or any number of amino acids comprising at least one

CC glycosylation consensus site, can be inserted into expression vectors

CC which in turn can be used to transform fungal host cells. The fungal

CC cells are then cultured and the insulin expressed in such cells can be

CC harvested

XX

SQ Sequence 86 AA;

Query Match 100.0%; Score 463; DB 2; Length 86;
 Best Local Similarity 100.0%; Pred. No. 1.5e-43;
 Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60
          |||
Db      1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60

Qy      61 SLQKRGIVEQCCTSICSLYQLENYCN 86
          |||
Db      61 SLQKRGIVEQCCTSICSLYQLENYCN 86
```

RESULT 3

AA42858

ID AA42858 standard; protein; 86 AA.

XX

AC AA42858;

XX

DT 19-JAN-2000 (first entry)

XX

DE Human insulin precursor, SEQ ID 5.

XX

KW Insulin; precursor; growth hormone; chaperone; intramolecular; folding;
 KW conformation; chimeric protein; cleavable; recombinant; production;
 KW yield.

XX

OS Homo sapiens.

XX

PN WO9950302-A1.

XX

PD 07-OCT-1999.

XX

PF 31-MAR-1998; 98WO-CN000052.

XX

PR 31-MAR-1998; 98WO-CN000052.

XX

PA (TONG-) TONGHUA GANTECH BIOTECHNOLOGY LTD.

XX

PI Gan Z;

XX

DR WPI; 1999-610839/52.

XX

PT New chimeric proteins containing human growth hormone fragment, used
 PT particularly for the production of human insulin.

XX

PS Claim 10; Page 29; 46pp; English.

XX

CC This sequence represents a human insulin precursor comprising insulin A
 CC and B chains separated by a 34 residue peptide sequence. This insulin
 CC precursor can be a component of chimeric proteins which additionally
 CC contains an N-terminal fragment of human growth hormone (hGH) and a
 CC cleavable peptide linker (AA42857). The hGH portion of the chimeric
 CC protein acts as an intramolecular chaperone (IMC) for the insulin
 CC precursor, enabling it to fold correctly. The cleavable peptide linker
 CC has a C-terminal Arg residue which enables the hGH portion of the
 CC chimeric protein to be removed after folding has taken place. Production

XX 06-JAN-1999; 99US-0115010P.
XX
PA (GETH) GENENTECH INC.
XX
PI Dubaquié Y, Lowman H;
XX
DR WPI; 2000-465955/40.
XX
PT Novel insulin-like growth factor (IGF) 1 mutants that selectively bind to
PT IGF binding protein (IGFBP)-1 or IGFBP-3, used to improve the half-lives
PT of IGF-I and insulin.
XX
PS Disclosure; Page 44; 48pp; English.
XX
CC The present invention describes an insulin-like growth factor (IGF)-1
CC variant (I), where an amino acid at position 3, 4, 5, 7, 10, 14, 17, 23,
CC 24, 25, 43, 49 or 63, optionally in combination with an amino acid at
CC position 12 and/or 16 of the native human IGF-1 sequence, is replaced
CC with an alanine, glycine, or a serine residue. The residue at position 7
CC may be replaced by any amino acid. (I) can have antidiabetic, cardiant,
CC neuroprotective, anorectic, tranquilliser, vulnerary, anorectic,
CC nephrotropic, dermatological, antiHIV and antiviral activities. The IGF-1
CC mutants are used in any methods where IGFs or insulin are used, e.g. in
CC treating hyperglycaemia, obesity-related, neurological, cardiac, renal,
CC immunological, and anabolic disorders. These disorders include lung
CC diseases, glomerulonephritis, interstitial nephritis, Turner's syndrome,
CC Laron's syndrome, short stature, increased fat mass-to-lean ratios,
CC immunological disorders, peripheral neuropathy, multiple sclerosis,
CC muscular dystrophy, catabolic states, trauma, wounding, infection, human
CC immunodeficiency virus (HIV), wounds, skin disorders, diabetes, heart
CC dysfunctions, kidney disorders, and whole body growth disorders. They can
CC also be used for increasing serum and tissue levels of biological active
CC IGF or insulin a mammal. The IGF-1 mutants improve the half-lives of IGF-
CC 1 and insulin. The present sequence represents the native human
CC proinsulin protein sequence, which is given in the exemplification of the
CC present invention
XX
SQ Sequence 86 AA;

RESULT 5
AAM48218
ID AAM48218 standard; protein; 86 AA.
XX

AC AAM48218;
 XX
 DT 18-MAR-2002 (first entry)
 XX
 DE Human proinsulin.
 XX
 KW Antirheumatic; antiarthritic; osteopathic; cartilage disorder;
 KW insulin-like growth factor; IGF; binding protein; IGFBP;
 KW rheumatoid arthritis; osteoarthritis; proinsulin; human.
 XX
 OS Homo sapiens.
 XX
 PN WO200187323-A2.
 XX
 PD 22-NOV-2001.
 XX
 PF 16-MAY-2001; 2001WO-US015904.
 XX
 PR 16-MAY-2000; 2000US-0204490P.
 PR 15-NOV-2000; 2000US-0248985P.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Dubaquie Y, Filvaroff EH, Lowman HB;
 XX
 DR WPI; 2002-082942/11.
 XX
 PT Treating cartilage disorders including cartilage damage by injury or
 PT degenerative cartilagenous disorders, by contacting cartilage with
 PT insulin-like growth factor analog with altered affinity for IGF-binding
 PT proteins.
 XX
 PS Disclosure; Fig 16; 136pp; English.
 XX
 CC The present invention relates to a method for treating cartilage
 CC disorders. The method comprises contacting cartilage with an active agent
 CC such as insulin-like growth factor (IGF-1) analog with a binding affinity
 CC preference for IGF binding protein-3 (IGFBP-3) over IGFBP-1, an IGF-1
 CC analog with a binding affinity preference for IGFBP-1 over IGFBP-3, or a
 CC IGFBP displacer peptide that prevents the interaction of IGF with an
 CC IGFBP and does not bind to human IGF receptor. The method is useful for
 CC treating cartilage disorders (CD), including degenerative CD, articular
 CC CD such as rheumatoid arthritis and osteoarthritis. The present sequence
 CC is human proinsulin, which was used to illustrate the invention
 XX
 SQ Sequence 86 AA;

Query Match 100.0%; Score 463; DB 5; Length 86;
 Best Local Similarity 100.0%; Pred. No. 1.5e-43;
 Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Qy 61 SLQKRGIVEQCCTSICSLYQLENYCN 86
 ||||||||||||||||||||||||||||

RESULT 6

ADC64463

ID ADC64463 standard; protein; 86 AA.

XX

AC ADC64463;

XX

DT 18-DEC-2003 (first entry)

XX

DE Amino acid sequence for human proinsulin.

XX

KW Immunoassay; human C-peptide; HCP; immune complex; human; proinsulin.

XX

OS Homo sapiens.

XX

PN US2002160435-A1.

XX

PD 31-OCT-2002.

XX

PF 12-JUN-2001; 2001US-00878380.

XX

PR 12-JUN-2000; 2000JP-00174691.

XX

PA (KITA/) KITAJIMA S.

PA (KURA/) KURANO Y.

PA (NAKA/) NAKATSUBO K.

PA (NISH/) NISHIZONO I.

XX

PI Kitajima S, Kurano Y, Nakatsubo K, Nishizono I;

XX

DR WPI; 2003-765139/72.

XX

PT Measuring human C-peptide, by reacting sample C-peptide with two
PT different human C-peptide antibodies that recognize different epitopes on
PT peptide, to form immune complex, separating and quantifying immune
PT complex.

XX

PS Disclosure; SEQ ID NO 1; 20pp; English.

XX

CC The present invention relates to an immunoassay for measuring human C-
CC peptide (HCP). The method comprises reacting HCP in a sample with a first
CC anti-HCP antibody and a second anti-HCP antibody which is immobilised on
CC a support, to form an immune complex, and separating and quantifying the
CC immune complex, where the first and second antibody recognises the
CC epitope existing in the region from 1-110 and 1-16 amino acid residues,
CC respectively, from the N-terminal end of HCP. Also disclosed is a kit for
CC measuring human C-peptide. The method is useful for measuring human C-
CC peptides. The method provides high reproducibility, high detection
CC sensitivity, and low cross-reactivity to proinsulin. The present sequence
CC represents the amino acid sequence for human proinsulin.

XX

SQ Sequence 86 AA;

Query Match 100.0%; Score 463; DB 7; Length 86;
Best Local Similarity 100.0%; Pred. No. 1.5e-43;

Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60
          |||
Db      1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60

Qy      61 SLQKRGIVEQCCTSICSLYQLENYCN 86
          |||
Db      61 SLQKRGIVEQCCTSICSLYQLENYCN 86
```

RESULT 7

ADF16632

ID ADF16632 standard; protein; 86 AA.

XX

AC ADF16632;

XX

DT 12-FEB-2004 (first entry)

XX

DE Human albumin fusion protein-related protein SeqID1734.

XX

KW albumin fusion protein; albumin activity; human serum albumin;

KW serum osmotic pressure; shelf-life; stability; antidiabetic;

KW gene therapy; diabetes mellitus; human; gene; ds.

XX

OS Homo sapiens.

XX

PN WO2003060071-A2.

XX

PD 24-JUL-2003.

XX

PF 23-DEC-2002; 2002WO-US040891.

XX

PR 21-DEC-2001; 2001US-0341811P.

PR 24-JAN-2002; 2002US-0350358P.

PR 28-JAN-2002; 2002US-0351360P.

PR 26-FEB-2002; 2002US-0359370P.

PR 28-FEB-2002; 2002US-0360000P.

PR 27-MAR-2002; 2002US-0367500P.

PR 08-APR-2002; 2002US-0370227P.

PR 10-MAY-2002; 2002US-0378950P.

PR 24-MAY-2002; 2002US-0382617P.

PR 28-MAY-2002; 2002US-0383123P.

PR 05-JUN-2002; 2002US-0385708P.

PR 10-JUL-2002; 2002US-0394625P.

PR 24-JUL-2002; 2002US-0398008P.

PR 09-AUG-2002; 2002US-0402131P.

PR 13-AUG-2002; 2002US-0402708P.

PR 18-SEP-2002; 2002US-0411355P.

PR 18-SEP-2002; 2002US-0411426P.

PR 02-OCT-2002; 2002US-0414984P.

PR 11-OCT-2002; 2002US-0417611P.

PR 23-OCT-2002; 2002US-0420246P.

PR 05-NOV-2002; 2002US-0423623P.

XX

PA (HUMA-) HUMAN GENOME SCI INC.

PA (DELZ) DELTA BIOTECHNOLOGY LTD.

PA (PRIN-) PRINCIPIA PHARM CORP.
 XX
 PI Ballance DJ, Turner AJ, Rosen CA, Haseltine WA;
 XX
 DR WPI; 2003-598517/56.
 DR N-PSDB; ADF16306.
 XX
 PT New albumin fusion protein, useful for preparing a composition for
 PT treating diabetes mellitus.
 XX
 PS Example 4; SEQ ID NO 1734; 24pp; English.
 XX
 CC This invention relates to a novel albumin fusion protein having albumin
 CC or biological activity. Human serum albumin is responsible for a
 CC significant proportion of the osmotic pressure of serum and also
 CC functions as a carrier of endogenous and exogenous ligands. The fusion of
 CC albumin to a therapeutic protein may increase shelf-life and stability of
 CC the therapeutic protein. The albumin fusion protein of the invention may
 CC allow production of compositions with antidiabetic activity whilst the
 CC nucleotide sequence which encodes it may be useful for gene therapy. The
 CC albumin fusion protein is useful for preparing a composition for treating
 CC diabetes mellitus. The present sequence is that of a therapeutic protein
 CC which was fused with human albumin to create a novel albumin fusion
 CC protein of the invention. Note: The sequence data for this patent did not
 CC form part of the printed specification, but was obtained in electronic
 CC format directly from WIPO at ftp.wipo.int/pub/publishedpct_sequences
 XX
 SQ Sequence 86 AA;

Query Match 100.0%; Score 463; DB 7; Length 86;
 Best Local Similarity 100.0%; Pred. No. 1.5e-43;
 Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60
 Qy 61 SLQKRGIVEQCCTSICSLYQLENYCN 86
 ||||||||||||||||||||||||||||
 Db 61 SLQKRGIVEQCCTSICSLYQLENYCN 86

RESULT 8
 ADH21860

ID ADH21860 standard; protein; 86 AA.
 XX
 AC ADH21860;
 XX
 DT 11-MAR-2004 (first entry)
 XX
 DE Human long-acting insulin peptide, SEQ ID NO:657.
 XX
 KW Fusion protein; human serum albumin; HSA; therapeutic protein;
 KW shelf-life; in vitro biological activity; in vivo biological activity;
 KW metabolic disorder; endocrine disorder; diabetes; type 1; type 2;
 KW diabetes-related condition; hyperglycaemia; neural disorder; neuropathy;
 KW retinopathy; cardiovascular disorder; heart disease; renal disorder;

KW obesity; glucose level maintenance; weight loss; antidiabetic; cardiant;
 KW anorectic; ophthalmological; gene therapy.
 XX
 OS Homo sapiens.
 XX
 PN WO2003059934-A2.
 XX
 PD 24-JUL-2003.
 XX
 PF 23-DEC-2002; 2002WO-US040892.
 XX
 PR 21-DEC-2001; 2001US-0341811P.
 PR 24-JAN-2002; 2002US-0350358P.
 PR 26-FEB-2002; 2002US-0359370P.
 PR 28-FEB-2002; 2002US-0360000P.
 PR 27-MAR-2002; 2002US-0367500P.
 PR 08-APR-2002; 2002US-0370227P.
 PR 10-MAY-2002; 2002US-0378950P.
 PR 24-JUL-2002; 2002US-0398008P.
 PR 09-AUG-2002; 2002US-0402131P.
 PR 13-AUG-2002; 2002US-0402708P.
 PR 18-SEP-2002; 2002US-0411355P.
 PR 02-OCT-2002; 2002US-0414984P.
 PR 11-OCT-2002; 2002US-0417611P.
 PR 23-OCT-2002; 2002US-0420246P.
 PR 05-NOV-2002; 2002US-0423623P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Rosen CA, Haseltine WA;
 XX
 DR WPI; 2003-598501/56.
 DR N-PSDB; ADH21708.
 XX
 PT New albumin fusion protein, useful for preparing a composition for
 PT treating diabetes mellitus.
 XX
 PS Disclosure; SEQ ID NO 657; 1086pp; English.
 XX
 CC The invention relates to fusion proteins comprising human serum albumin
 CC (ADH21530) and a therapeutic polypeptide such as a therapeutic protein,
 CC antibody or peptide or their variants or fragments. The therapeutic
 CC protein may be fused to the N-terminus, the C-terminus or both termini of
 CC albumin via a linker. The albumin component of the fusion proteins
 CC prolongs the shelf-life and the in vitro and vivo biological activity of
 CC the proteins compared with those of the corresponding therapeutic
 CC proteins on their own. The invention also relates to nucleic acids
 CC encoding albumin fusion proteins, vectors and host cells comprising an
 CC albumin fusion protein nucleic acid, compositions and kits comprising an
 CC albumin fusion protein, the method of extending the shelf-life of a
 CC therapeutic protein by fusion with albumin, and the treatment of disease
 CC using an albumin fusion protein. The albumin fusion proteins may be used
 CC in the treatment of metabolic/endocrine disorders, diabetes and diabetes-
 CC related conditions. Specifically the albumin fusion proteins may be used
 CC to treat type 1 and type 2 diabetes, hyperglycaemia, neural disorders
 CC (especially neuropathy), retinopathy, cardiovascular disorders
 CC (especially heart disease, renal disorders and obesity. The proteins may

CC also be used in a method of maintaining a basal glucose level in a
CC patient and in a method for losing weight. The present sequence is
CC related to the invention.

XX

SQ Sequence 86 AA;

Query Match 100.0%; Score 463; DB 7; Length 86;
Best Local Similarity 100.0%; Pred. No. 1.5e-43;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60
|||||

Db 1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60

Qy 61 SLQKRGIVEQCCTSICSLYQLENYCN 86
|||||

Db 61 SLQKRGIVEQCCTSICSLYQLENYCN 86

RESULT 9

ADT93277

ID ADT93277 standard; protein; 86 AA.

XX

AC ADT93277;

XX

DT 16-DEC-2004 (first entry)

XX

DE Human native proinsulin protein.

XX

KW antidiabetic; nephrotropic; cardiovascular; hepatotropic; anabolic;

KW gene therapy; insulin-like growth factor-I; IGF-I; dysregulation;

KW GH/IGF axis; hyperglycemic disorder; renal disorder;

KW congestive heart failure; hepatic failure; poor nutrition;

KW wasting syndrome; catabolic state; IGF binding protein-1; IGFBP-1;

KW renal failure; proinsulin.

XX

OS Homo sapiens.

XX

PN AU2003236454-A1.

XX

PD 18-SEP-2003.

XX

PF 22-AUG-2003; 2003AU-00236454.

XX

PR 22-AUG-2003; 2003AU-00236454.

XX

PA (GETH) GENENTECH INC.

XX

PI Mortensen DL, Lowman HB, Fielder PJ, Dubaquié Y;

XX

DR WPI; 2004-662617/65.

XX

PT New insulin-like growth factor-I (IGF-I) variant, useful for treating

PT disorder associated with dysregulation of GH(growth hormone)/IGF axis

PT e.g. renal disorder.

XX

PS Disclosure; SEQ ID NO 2; 61pp; English.

PR 02-JAN-1982; 82US-00222010.
 PR 03-MAR-1982; 82US-00354287.
 XX
 PA (UYNY-) STATE UNIV NEW YORK.
 XX
 PI Inouye M, Nakamura K;
 XX
 DR WPI; 1982-59775E/29.
 DR N-PSDB; AAN20041.
 XX
 PT Plasmid cloning vehicles - useful for transforming bacterial hosts to
 PT produce eukaryotic polypeptide(s).
 XX
 PS Disclosure; Fig 27; 114pp; English.
 XX
 CC The sequence comprises human proinsulin. (Updated on 25-MAR-2003 to
 CC correct PR field.)
 XX
 SQ Sequence 87 AA;

Query Match 100.0%; Score 463; DB 1; Length 87;
 Best Local Similarity 100.0%; Pred. No. 1.5e-43;
 Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60
 |
 Db 2 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 61

 Qy 61 SLQKRGIVEQCCTSICSLYQLENYCN 86
 |
 Db 62 SLQKRGIVEQCCTSICSLYQLENYCN 87

RESULT 11

AAP40217

ID AAP40217 standard; protein; 87 AA.

XX

AC AAP40217;

XX

DT 25-MAR-2003 (revised)

DT 12-FEB-1992 (first entry)

XX

DE Sequence of the 32 N-terminal AAs of proinsulin.

XX

KW Hormone; cloning vector; phage resistant.

XX

OS Homo sapiens.

XX

FH	Key	Location/Qualifiers
----	-----	---------------------

FT	Region	2. .31
----	--------	--------

FT		/label= B-chain
----	--	-----------------

FT	Region	32. .66
----	--------	---------

FT		/label= C-chain
----	--	-----------------

FT	Region	67. .87
----	--------	---------

FT		/label= A-chain
----	--	-----------------

XX

PN GB2126237-A.

XX
 PD 21-MAR-1984.
 XX
 PF 01-SEP-1983; 83GB-00023468.
 XX
 PR 03-SEP-1982; 82US-00414290.
 PR 05-SEP-1984; 84US-00647338.
 XX
 PA (ELIL) LILLY & CO ELI.
 XX
 PI Hershberge CL, Rosteck PR;
 XX
 DR WPI; 1984-070793/12.
 DR N-PSDB; AAN40179.
 XX
 PT Protecting bacteria from phage infection - by transformation with cloning
 PT vector contg. segment with restriction and modification activity.
 XX
 PS Example; Fig 10; 28pp; English.
 XX
 CC Plasmid pTh alpha 1 was constructed by inserting a synthesised gene for
 CC thymosin alpha 1 (AAN40178) into plasmid pBR322. It is used for the
 CC construction of pTrp24. The inventors claim a method for protecting
 CC bacteria from phage infection - by transformation with cloning vector
 CC contg. segment with restriction and modification activity. Prodn. of
 CC plasmid pPR 26 or pPR27 which uses pTrp24; and prodn. of plasmid pPR29
 CC which uses a synthetic gene coding for the 32 N-terminal AAs of
 CC proinsulin (see AAN40179). (Updated on 25-MAR-2003 to correct PA field.)
 XX
 SQ Sequence 87 AA;

Query Match 100.0%; Score 463; DB 1; Length 87;
 Best Local Similarity 100.0%; Pred. No. 1.5e-43;
 Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60
 |||||
 Db 2 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 61
 Qy 61 SLQKRGIVEQCCTSICSLYQLENYCN 86
 |||||
 Db 62 SLQKRGIVEQCCTSICSLYQLENYCN 87

RESULT 12

AAP50127

ID AAP50127 standard; protein; 87 AA.

XX

AC AAP50127;

XX

DT 25-MAR-2003 (revised)

DT 16-AUG-2002 (revised)

DT 30-SEP-1991 (first entry)

XX

DE Sequence of the 32 N-terminal AAs of proinsulin.

XX

KW Selectable vector; autonomously replicating vector; expression vector.

XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Region 2. .31
 FT /label= A chain
 FT Region 32. .66
 FT /label= B chain
 FT Region 67. .87
 FT /label= A chain
 XX
 PN EP154539-A.
 XX
 PD 11-SEP-1985.
 XX
 PF 04-MAR-1985; 85EP-00301469.
 XX
 PR 06-MAR-1984; 84US-00586592.
 XX
 PA (ELIL) LILLY & CO ELI.
 XX
 PI Schoner R, Schoner B;
 XX
 DR WPI; 1985-224921/37.
 DR N-PSDB; AAN50152.
 XX
 PT New recombinant DNA expression vector - with autonomous replication and
 PT on transcription generating polycistronic mrna.
 XX
 PS Example; Fig 14; 118pp; English.
 XX
 CC The inventors claim a process for preparing selectable and autonomously
 CC replicating recombinant DNA expression vectors which comprise 1) a
 CC transcriptional and translational activating sequence which is in the
 CC reading frame of a nucleotide sequence which codes for a peptide or
 CC polypeptide; 2) a translational stop signal; 3) a translational start
 CC signal which is in the reading frame of a nucleotide sequence that codes
 CC for a functional polypeptide; and 4) an additional translational stop
 CC signal. The peptide or polypeptide coding sequence codes for 2-20 AAs,
 CC esp. AAP50122-P50125. The functional polypeptide is esp. growth hormone,
 CC human insulin, interferon and human tissue plasminogen activator.
 CC (Updated on 16-AUG-2002 to add missing OS field.) (Updated on 25-MAR-2003
 CC to correct PA field.)
 XX
 SQ Sequence 87 AA;

Query Match 100.0%; Score 463; DB 1; Length 87;
 Best Local Similarity 100.0%; Pred. No. 1.5e-43;
 Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 2 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 61
 Qy 61 SLQKRGIVEQCCTSICSLYQLENYCN 86
 ||||||||||||||||||||||||

RESULT 13

AAP50060

ID AAP50060 standard; protein; 87 AA.

XX

AC AAP50060;

XX

DT 25-MAR-2003 (revised)

DT 16-AUG-2002 (revised)

DT 11-NOV-1991 (first entry)

XX

DE Synthetic proinsulin.

XX

KW Proinsulin; vector; proteinaceous granule.

XX

OS Homo sapiens.

XX

Key	Location/Qualifiers
-----	---------------------

FT Region	1. .30
-----------	--------

FT	/label= B chain.
----	------------------

FT Region	31. .65
-----------	---------

FT	/label= C chain.
----	------------------

FT Region	66. .86
-----------	---------

FT	/label= A chain.
----	------------------

XX

PN EP159123-A.

XX

PD 23-OCT-1985.

XX

PF 04-MAR-1985; 85EP-00301468.

XX

PR 06-MAR-1984; 84US-00586582.

PR 26-JUL-1984; 84US-00634920.

PR 31-JAN-1985; 85US-00697090.

XX

PA (ELIL) LILLY & CO ELI.

XX

PI Hsiung HM, Schoner RG, Schoner BE;

XX

DR WPI; 1985-265090/43.

DR N-PSDB; AAN50082.

XX

PT New selectable and autonomously replicating DNA expression vector -
PT useful in producing proteinaceous granules in cell transformants, esp.
PT for prodn. of bovine growth hormone derivs.

XX

PS Disclosure; Fig 14; 115pp; English.

XX

CC The synthetic proinsulin gene is expressed in a new selectable and
CC autonomously replicating recombinant DNA expression vector comprising a
CC runaway replicon and a transcriptional and translational activating
CC sequence in the reading frame of the proinsulin coding sequence, the
CC sequence contg. a translational stop signal. Host cells contg. the
CC vector, which is esp. plasmid pCZ103, are cultured, and proinsulin is
CC produced as a highly homogeneous species of proteinaceous granule. The

CC granule can be readily isolated from cell lysates and is stable on
CC washing with urea or detergent solns. at low concns. The granule contains
CC at least 50% of proinsulin and all isolation operations are simplified.
CC (Updated on 16-AUG-2002 to add missing OS field.) (Updated on 25-MAR-2003
CC to correct PA field.)
XX
SQ Sequence 87 AA;

Query Match 100.0%; Score 463; DB 1; Length 87;
Best Local Similarity 100.0%; Pred. No. 1.5e-43;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60
|
Db 2 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 61

Qy 61 SLQKRGIVEQCCTSICSLYQLENYCN 86
|
Db 62 SLQKRGIVEQCCTSICSLYQLENYCN 87

RESULT 14

AAP61090

ID AAP61090 standard; protein; 87 AA.

XX

AC AAP61090;

XX

DT 28-FEB-1992 (first entry)

XX

DE Sequence encoded by the structural gene for human proinsulin.

XX

KW Recombinant plasmid; E.coli expression vector; secretion vector.

XX

OS Homo sapiens.

XX

PN US4624926-A.

XX

PD 25-NOV-1986.

XX

PF 03-MAR-1982; 82US-00354287.

XX

PR 02-JAN-1981; 81US-00222010.

PR 23-JUL-1981; 81US-00286070.

XX

PA (UYNY-) UNIV OF NEW YORK.

XX

PI Inouye M, Nakamura K;

XX

DR WPI; 1986-331802/50.

DR N-PSDB; AAN60872.

XX

PT New recombinant plasmid(s) - contg. DNA sequences encoding exogenous
PT polypeptide and outer membrane protein of E coli.

XX

PS Example; Fig 27; 44pp; English.

XX

CC The inventors claim new recombinant plasmids contg. a DNA sequence

XX
 PS Disclosure; Fig 2b; 58pp; English.
 XX
 CC This sequence represents human proinsulin and was decoded from the
 CC sequences given in AAQ36996-7001. The cDNA fragment coding for proinsulin
 CC was inserted into plasmid vector pUC19 and digested with KpnI and
 CC HindIII. This resulted in the formation of the vector pPINS. A fragment
 CC encoding amino acids 1-73 of CAT (see AAQ37002) was inserted into pPINS
 CC to give a plasmid which contained DNA sequences which coded for amino
 CC acids 1-73 of CAT, an 8 amino acid linker sequence and human proinsulin.
 CC This plasmid, pUC-CAT-proinsulin, could be used in the formation of
 CC insulin analogues which may be used in the treatment of types I and II
 CC diabetes. (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 87 AA;

Query Match 100.0%; Score 463; DB 2; Length 87;
 Best Local Similarity 100.0%; Pred. No. 1.5e-43;
 Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60
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 Db 2 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 61
 Qy 61 SLQKRGIVEQCCTSICSLYQLENYCN 86
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 Db 62 SLQKRGIVEQCCTSICSLYQLENYCN 87

Search completed: March 9, 2005, 04:10:15
 Job time : 92.8081 secs

OM protein - protein search, using sw model

Run on: March 9, 2005, 04:04:46 ; Search time 23.1661 Seconds
 (without alignments)
 277.122 Million cell updates/sec

Title: US-10-054-873-4
 Perfect score: 463
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Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Issued_Patents_AA:*
 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
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 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
 5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	%		DB	ID	Description
		Query	Match Length			
1	463	100.0	86	4	US-09-477-924-2	Sequence 2, Appli
2	463	100.0	86	4	US-09-723-981-2	Sequence 2, Appli
3	463	100.0	86	4	US-09-723-896-2	Sequence 2, Appli
4	463	100.0	86	4	US-09-878-380-1	Sequence 1, Appli
5	463	100.0	96	2	US-09-134-836-4	Sequence 4, Appli
6	463	100.0	96	3	US-09-386-303A-4	Sequence 4, Appli
7	463	100.0	96	4	US-09-947-563-4	Sequence 4, Appli
8	463	100.0	97	1	US-08-160-376A-4	Sequence 4, Appli
9	463	100.0	110	3	US-08-950-720A-11	Sequence 11, Appli
10	463	100.0	110	3	US-08-589-028-2	Sequence 2, Appli
11	463	100.0	110	3	US-08-784-582-2	Sequence 2, Appli

12	463	100.0	110	3	US-08-785-271-2	Sequence 2, Appli
13	463	100.0	110	4	US-08-472-701-2	Sequence 2, Appli
14	463	100.0	110	4	US-09-185-852-2	Sequence 2, Appli
15	463	100.0	110	4	US-09-815-229-3	Sequence 3, Appli
16	463	100.0	110	4	US-09-617-389B-20	Sequence 20, Appl
17	463	100.0	110	4	US-09-323-738-2	Sequence 2, Appli
18	463	100.0	110	4	US-09-015-399-7	Sequence 7, Appli
19	463	100.0	110	5	PCT-US95-08596-2	Sequence 2, Appli
20	463	100.0	117	4	US-09-280-030-63	Sequence 63, Appl
21	463	100.0	130	4	US-09-280-030-62	Sequence 62, Appl
22	463	100.0	151	2	US-08-508-664-15	Sequence 15, Appl
23	463	100.0	161	2	US-08-508-664-16	Sequence 16, Appl
24	463	100.0	167	1	US-07-918-953-8	Sequence 8, Appli
25	463	100.0	167	1	US-08-081-661-8	Sequence 8, Appli
26	457	98.7	96	2	US-09-134-836-5	Sequence 5, Appli
27	457	98.7	96	3	US-09-386-303A-5	Sequence 5, Appli
28	457	98.7	96	4	US-09-947-563-5	Sequence 5, Appli
29	457	98.7	97	1	US-08-389-487-7	Sequence 7, Appli
30	456	98.5	90	1	US-08-030-731A-43	Sequence 43, Appl
31	456	98.5	98	4	US-09-701-968-7	Sequence 7, Appli
32	456	98.5	99	4	US-09-701-968-8	Sequence 8, Appli
33	456	98.5	100	4	US-09-701-968-9	Sequence 9, Appli
34	449	97.0	110	4	US-09-574-443-1	Sequence 1, Appli
35	446	96.3	97	3	US-09-099-307-6	Sequence 6, Appli
36	444	95.9	97	3	US-09-099-307-8	Sequence 8, Appli
37	443	95.7	110	3	US-08-589-028-4	Sequence 4, Appli
38	443	95.7	110	3	US-08-784-582-4	Sequence 4, Appli
39	443	95.7	110	3	US-08-785-271-4	Sequence 4, Appli
40	440	95.0	97	3	US-09-099-307-7	Sequence 7, Appli
41	435	94.0	97	3	US-09-099-307-11	Sequence 11, Appl
42	398	86.0	91	4	US-09-676-787-7	Sequence 7, Appli
43	300	64.8	56	4	US-09-815-229-10	Sequence 10, Appl
44	292.5	63.2	67	3	US-08-981-988A-1	Sequence 1, Appli
45	290.5	62.7	83	3	US-08-981-988A-3	Sequence 3, Appli

ALIGNMENTS

```

RESULT 1
US-09-477-924-2
; Sequence 2, Application US/09477924
; Patent No. 6403764
; GENERAL INFORMATION:
; APPLICANT: Dubaquie, Yves
; APPLICANT: Lowman, Henry
; TITLE OF INVENTION: PROTEIN VARIANTS
; FILE REFERENCE: P1712R1-1
; CURRENT APPLICATION NUMBER: US/09/477,924
; CURRENT FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 6
; SEQ ID NO 2
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-477-924-2

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Query Match 100.0%; Score 463; DB 4; Length 86;
Best Local Similarity 100.0%; Pred. No. 2.4e-47;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60
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Db 1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60

Qy 61 SLQKRGIVEQCCTSICSLYQLENYCN 86
|
Db 61 SLQKRGIVEQCCTSICSLYQLENYCN 86

RESULT 2

US-09-723-981-2
; Sequence 2, Application US/09723981
; Patent No. 6506874
; GENERAL INFORMATION:
; APPLICANT: Dubaquie, Yves
; APPLICANT: Lowman, Henry
; TITLE OF INVENTION: PROTEIN VARIANTS
; FILE REFERENCE: P1712R1
; CURRENT APPLICATION NUMBER: US/09/723,981
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 09/477,923
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 6
; SEQ ID NO 2
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-723-981-2

Query Match 100.0%; Score 463; DB 4; Length 86;
Best Local Similarity 100.0%; Pred. No. 2.4e-47;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60
|
Db 1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60

Qy 61 SLQKRGIVEQCCTSICSLYQLENYCN 86
|
Db 61 SLQKRGIVEQCCTSICSLYQLENYCN 86

RESULT 3

US-09-723-896-2
; Sequence 2, Application US/09723896
; Patent No. 6509443
; GENERAL INFORMATION:
; APPLICANT: Dubaquie, Yves
; APPLICANT: Lowman, Henry
; TITLE OF INVENTION: PROTEIN VARIANTS
; FILE REFERENCE: P1712R1
; CURRENT APPLICATION NUMBER: US/09/723,896
; CURRENT FILING DATE: 2000-11-28

RESULT 5

US-09-134-836-4

; Sequence 4, Application US/09134836

; Patent No. 5986048

; GENERAL INFORMATION:

; APPLICANT: Rubroder, Franz-Josef

; APPLICANT: Keller, Reinhold

; TITLE OF INVENTION: Improved process for obtaining

; TITLE OF INVENTION: insulin precursors having correctly bonded cystine bridges

; NUMBER OF SEQUENCES: 7

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Finnegan, Henderson, Farrahaw, Garrett &

; ADDRESSEE: Dunner

; STREET: 1300 I Street, N.W.

; CITY: Washington

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20005-3315

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/134,836

; FILING DATE:

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Leslie McDonell

; REGISTRATION NUMBER: 34,872

; REFERENCE/DOCKET NUMBER: 02481.1600-00000

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202) 408-4000

; TELEFAX: (202) 408-4400

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 96 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; ORIGINAL SOURCE:

; ORGANISM: Escherichia coli

; FEATURE:

; NAME/KEY: Protein

; LOCATION: 1..96

US-09-134-836-4

Query Match 100.0%; Score 463; DB 2; Length 96;

Best Local Similarity 100.0%; Pred. No. 2.8e-47;

Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db          11 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 70
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Db          71 SLQKRGIVEQCCTSICSLYQLENYCN 96

```

RESULT 6

US-09-386-303A-4

; Sequence 4, Application US/09386303A

; Patent No. 6380355

; GENERAL INFORMATION:

; APPLICANT: Rubroder, Franz-Josef

; Keller, Reinhold

; TITLE OF INVENTION: Improved process for obtaining

insulin precursors having correctly bonded cystine
bridges

; NUMBER OF SEQUENCES: 7

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Finnegan, Henderson, Farrabow, Garrett &

; Dunner

; STREET: 1300 I Street, N.W.

; CITY: Washington

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20005-3315

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/386,303A

; FILING DATE: 31-Aug-1999

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/134,836

; FILING DATE: <Unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: Leslie McDonell

; REGISTRATION NUMBER: 34,872

; REFERENCE/DOCKET NUMBER: 02481.1600-00000

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202) 408-4000

; TELEFAX: (202) 408-4400

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 96 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; ORIGINAL SOURCE:

; ORGANISM: Escherichia coli

; FEATURE:

; NAME/KEY: Protein

; LENGTH: 96 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Escherichia coli
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..96
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-947-563-4

Query Match 100.0%; Score 463; DB 4; Length 96;
Best Local Similarity 100.0%; Pred. No. 2.8e-47;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60
 |||||
Db 11 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 70

Qy 61 SLQKRGIVEQCCTSICSLYQLENYCN 86
 |||||
Db 71 SLQKRGIVEQCCTSICSLYQLENYCN 96

RESULT 8

US-08-160-376A-4

; Sequence 4, Application US/08160376A
; Patent No. 5473049
; GENERAL INFORMATION:
; APPLICANT: Obermeier, Ranier
; APPLICANT: Gerl, Martin
; APPLICANT: Ludwig, Jurgen
; APPLICANT: Sabel, Walter
; TITLE OF INVENTION: Process For Obtaining Proinsulin
; TITLE OF INVENTION: Possessing Correctly Linked
; TITLE OF INVENTION: Cystine Bridges
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenneth A. Genoni, Esq.
; STREET: Rt. 202-206 No. 5473049th/P.O. Box 2500
; CITY: Somerville
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 08876-1258
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM 386
; OPERATING SYSTEM: WINDOWS 3.1
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/160,376A
; FILING DATE: December 1, 1993
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GE P 4240420.7

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; FILING DATE: December 2, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Barbara V. Maurer, Esq.
; REGISTRATION NUMBER: 31,287
; REFERENCE/DOCKET NUMBER: HOE 92/F 384
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 231-4079
; TELEFAX: (908) 231-2255
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 97 Amino Acids
; TYPE: Amino Acid (AA)
; TOPOLOGY: not relevant
US-08-160-376A-4
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Best Local Similarity 100.0%; Pred. No. 2.8e-47;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      61 SLQKRGIVEQCCTSICSLYQLENYCN 86
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Db      72 SLQKRGIVEQCCTSICSLYQLENYCN 97
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RESULT 9

US-08-950-720A-11

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; Sequence 11, Application US/08950720A
; Patent No. 6046028
; GENERAL INFORMATION:
; APPLICANT: Conklin, Darrell C.
; APPLICANT: Lofton-Day, Catherine E.
; APPLICANT: Lok, Si
; APPLICANT: Jaspers, Stephen R.
; TITLE OF INVENTION: INSULIN HOMOLOG
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/950,720A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
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; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sawislak, Deborah A
; REGISTRATION NUMBER: 37,438
; REFERENCE/DOCKET NUMBER: 96-09
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6672
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 110 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6046028e
US-08-950-720A-11

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Query Match          100.0%; Score 463; DB 3; Length 110;
Best Local Similarity 100.0%; Pred. No. 3.3e-47;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60
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Db      25 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 84

Qy      61 SLQKRGIVEQCCTSICSLYQLENYCN 86
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Db      85 SLQKRGIVEQCCTSICSLYQLENYCN 110

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RESULT 10

US-08-589-028-2

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; Sequence 2, Application US/08589028
; Patent No. 6087129

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; GENERAL INFORMATION:

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; APPLICANT: Newgard, Christopher B.
; APPLICANT: Halban, Philippe
; APPLICANT: No. 6087129mington, Karl D.
; APPLICANT: Clark, Samuel A.
; APPLICANT: Thigpen, Anice E.
; APPLICANT: Quaade, Christian
; APPLICANT: Kruse, Fred
; TITLE OF INVENTION: Recombinant Expression of Proteins From
; TITLE OF INVENTION: Secretory Cell Lines
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P. O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

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; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/589,028
; FILING DATE: Concurrently Herewith
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Highlander, Steven L.
; REGISTRATION NUMBER: 47,642
; REFERENCE/DOCKET NUMBER: UTSD:426\HYL
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 110 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-589-028-2

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Query Match          100.0%; Score 463; DB 3; Length 110;
Best Local Similarity 100.0%; Pred. No. 3.3e-47;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      25 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 84

Qy      61 SLQKRGIVEQCCTSICSLYQLENYCN 86
        ||||||||||||||||||||
Db      85 SLQKRGIVEQCCTSICSLYQLENYCN 110

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RESULT 11

US-08-784-582-2

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; Sequence 2, Application US/08784582
; Patent No. 6110707

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; GENERAL INFORMATION:

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; APPLICANT: Newgard, Christopher B.
; APPLICANT: Halban, Philippe A.
; APPLICANT: No. 6110707mington, Karl D.
; APPLICANT: Clark, Samuel A.
; APPLICANT: Thigpen, Anice E.
; APPLICANT: Quaade, Christian
; APPLICANT: Kruse, Fred
; APPLICANT: McGarry, Dennis
; TITLE OF INVENTION: RECOMBINANT EXPRESSION OF PROTEINS FROM
; TITLE OF INVENTION: SECRETORY CELL LINES
; NUMBER OF SEQUENCES: 79
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/784,582
; FILING DATE: Concurrently Herewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/028,427
; FILING DATE: 15-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/589,028
; FILING DATE: 19-JAN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Highlander, Steven L.
; REGISTRATION NUMBER: 37,642
; REFERENCE/DOCKET NUMBER: UTSD:514
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/418-3000
; TELEFAX: 512/474-7577
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 110 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-784-582-2

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Query Match          100.0%; Score 463; DB 3; Length 110;
Best Local Similarity 100.0%; Pred. No. 3.3e-47;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60
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Db      25 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 84

Qy      61 SLQKRGIVEQCCTSICSLYQLENYCN 86
        ||||||||||||||||||||||||
Db      85 SLQKRGIVEQCCTSICSLYQLENYCN 110

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RESULT 12

US-08-785-271-2

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; Sequence 2, Application US/08785271
; Patent No. 6194176
; GENERAL INFORMATION:
; APPLICANT: Newgard, Christopher B.
; APPLICANT: Halban, Philippe A.
; APPLICANT: No. 6194176mington, Karl D.
; APPLICANT: Clark, Samuel A.
; APPLICANT: Thigpen, Anice E.
; APPLICANT: Quaade, Christian
; APPLICANT: Kruse, Fred
; TITLE OF INVENTION: RECOMBINANT EXPRESSION OF PROTEINS FROM
; TITLE OF INVENTION: SECRETORY CELL LINES
; NUMBER OF SEQUENCES: 56

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; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/785,271
; FILING DATE: Concurrently Herewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/589,028
; FILING DATE: 19-JAN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Highlander, Steven L.
; REGISTRATION NUMBER: 37,642
; REFERENCE/DOCKET NUMBER: UTSD:513
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/418-3000
; TELEFAX: 512/474-7577
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 110 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-785-271-2

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Query Match          100.0%; Score 463; DB 3; Length 110;
Best Local Similarity 100.0%; Pred. No. 3.3e-47;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60
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Db      25 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 84
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Qy      61 SLQKRGIVEQCCTSICSLYQLENYCN 86
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Db      85 SLQKRGIVEQCCTSICSLYQLENYCN 110
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RESULT 13

US-08-472-701-2

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; Sequence 2, Application US/08472701
; Patent No. 6509165
; GENERAL INFORMATION:
; APPLICANT: Griffin, Ann C.
; APPLICANT: Hickey, William F.
; TITLE OF INVENTION: Detection and Treatment Methods for
; TITLE OF INVENTION: Type I Diabetes
; NUMBER OF SEQUENCES: 23

```

```

;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE:  LAHIVE & COCKFIELD
;   STREET:  60 State Street, suite 510
;   CITY:  Boston
;   STATE:  Massachusetts
;   COUNTRY:  USA
;   ZIP:  02109-1875
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE:  Floppy disk
;   COMPUTER:  IBM PC compatible
;   OPERATING SYSTEM:  PC-DOS/MS-DOS
;   SOFTWARE:  ASCII Text
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER:  US/08/472,701
;   FILING DATE:
;   CLASSIFICATION:  435
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:  US 08/272,220
;   FILING DATE:  08-JULY-1994
;   CLASSIFICATION:  435
;   ATTORNEY/AGENT INFORMATION:
;   NAME:  DeConti, Giulio A., Jr.
;   REGISTRATION NUMBER:  31,503
;   REFERENCE/DOCKET NUMBER:  DCI-092DV
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE:  (617)227-7400
;   TELEFAX:  (617)227-5941
;   INFORMATION FOR SEQ ID NO:  2:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH:  110 amino acids
;   TYPE:  amino acid
;   TOPOLOGY:  linear
;   MOLECULE TYPE:  protein
US-08-472-701-2

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Query Match          100.0%;  Score 463;  DB 4;  Length 110;
Best Local Similarity 100.0%;  Pred. No. 3.3e-47;
Matches   86;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

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Db      25 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 84
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Qy      61 SLQKRGIVEQCCTSICSLYQLENYCN 86
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RESULT 14

US-09-185-852-2

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; Sequence 2, Application US/09185852
; Patent No. 6537806
; GENERAL INFORMATION:
; APPLICANT: Osborne, William R.A.
; APPLICANT: Ramesh, Nagarajan
; TITLE OF INVENTION: Compositions and Methods for Treating Diabetes
; FILE REFERENCE: P-UW 3264

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; CURRENT APPLICATION NUMBER: US/09/185,852
; CURRENT FILING DATE: 1998-11-04
; EARLIER APPLICATION NUMBER: 60/087,660
; EARLIER FILING DATE: 1998-06-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-185-852-2

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Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      61 SLQKRGIVEQCCTSICSLYQLENYCN 86
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Db      85 SLQKRGIVEQCCTSICSLYQLENYCN 110
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RESULT 15

US-09-815-229-3

; Sequence 3, Application US/09815229
; Patent No. 6689747
; GENERAL INFORMATION:
; APPLICANT: Filvaroff, Ellen H.
; APPLICANT: Okumu, Franklin W.
; TITLE OF INVENTION: USE OF INSULIN FOR THE TREATMENT OF CARTILAGENOUS DISORDERS
; FILE REFERENCE: P1786R1US
; CURRENT APPLICATION NUMBER: US/09/815,229
; CURRENT FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: US 60/192,103
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 17
; SEQ ID NO 3
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-815-229-3

Query Match 100.0%; Score 463; DB 4; Length 110;
Best Local Similarity 100.0%; Pred. No. 3.3e-47;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      25 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 84

Qy      61 SLQKRGIVEQCCTSICSLYQLENYCN 86
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Db      85 SLQKRGIVEQCCTSICSLYQLENYCN 110
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Run on: March 9, 2005, 04:18:26 ; Search time 181.996 Seconds
(without alignments)
155.486 Million cell updates/sec

Title: US-10-054-873-4
Perfect score: 463
Sequence: 1 FVNQHLCGSHLVEALYLVCG.....IVEQCCTSICSLYQLENYCN 86

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Gapop 10.0 , Gapext 0.5

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	463	100.0	86	9	US-09-878-380-1	Sequence 1, Appli
2	463	100.0	86	10	US-09-858-935B-4	Sequence 4, Appli
3	463	100.0	86	13	US-10-028-410-2	Sequence 2, Appli
4	463	100.0	86	13	US-10-054-873-4	Sequence 4, Appli
5	463	100.0	86	14	US-10-444-326-2	Sequence 2, Appli
6	463	100.0	86	15	US-10-271-869-4	Sequence 4, Appli
7	463	100.0	86	15	US-10-444-262-2	Sequence 2, Appli
8	463	100.0	86	15	US-10-444-649-2	Sequence 2, Appli
9	463	100.0	86	15	US-10-444-701-2	Sequence 2, Appli
10	463	100.0	86	17	US-10-760-928-2	Sequence 2, Appli
11	463	100.0	87	17	US-10-869-040-89	Sequence 89, Appl
12	463	100.0	96	9	US-09-947-563-4	Sequence 4, Appli
13	463	100.0	110	9	US-09-205-658-125	Sequence 125, App
14	463	100.0	110	9	US-09-815-229-3	Sequence 3, Appli
15	463	100.0	110	9	US-09-804-409A-9	Sequence 9, Appli
16	463	100.0	110	10	US-09-969-748C-6	Sequence 6, Appli
17	463	100.0	110	10	US-09-963-693-125	Sequence 125, App
18	463	100.0	110	14	US-10-038-686-1	Sequence 1, Appli
19	463	100.0	110	14	US-10-328-813-2	Sequence 2, Appli
20	463	100.0	110	15	US-10-383-285-2	Sequence 2, Appli
21	463	100.0	110	15	US-10-346-563-2	Sequence 2, Appli
22	463	100.0	110	15	US-10-321-717-2	Sequence 2, Appli
23	463	100.0	110	15	US-10-411-037-44	Sequence 44, Appl
24	463	100.0	110	15	US-10-411-026-44	Sequence 44, Appl
25	463	100.0	110	15	US-10-410-962-44	Sequence 44, Appl
26	463	100.0	110	15	US-10-411-049-44	Sequence 44, Appl
27	463	100.0	110	15	US-10-700-725-20	Sequence 20, Appl
28	463	100.0	110	16	US-10-410-930-44	Sequence 44, Appl
29	463	100.0	110	16	US-10-410-997-44	Sequence 44, Appl
30	463	100.0	110	16	US-10-411-012-44	Sequence 44, Appl
31	463	100.0	110	16	US-10-287-994-44	Sequence 44, Appl
32	463	100.0	110	16	US-10-740-098-3	Sequence 3, Appli
33	463	100.0	110	16	US-10-410-913-44	Sequence 44, Appl
34	463	100.0	110	17	US-10-410-980-44	Sequence 44, Appl
35	463	100.0	110	17	US-10-869-040-7	Sequence 7, Appli
36	463	100.0	110	17	US-10-869-040-23	Sequence 23, Appl
37	463	100.0	110	17	US-10-869-040-26	Sequence 26, Appl
38	463	100.0	114	17	US-10-869-040-76	Sequence 76, Appl
39	463	100.0	117	9	US-09-280-030-63	Sequence 63, Appl
40	463	100.0	130	9	US-09-280-030-62	Sequence 62, Appl
41	463	100.0	257	17	US-10-869-040-196	Sequence 196, App
42	457	98.7	96	9	US-09-947-563-5	Sequence 5, Appli
43	456	98.5	110	17	US-10-869-040-21	Sequence 21, Appl
44	456	98.5	110	17	US-10-869-040-22	Sequence 22, Appl
45	442	95.5	110	16	US-10-419-539-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1

US-09-878-380-1

; Sequence 1, Application US/09878380

; Patent No. US20020160435A1

```
; GENERAL INFORMATION:
; APPLICANT: Fujirebio Inc.
; APPLICANT: KITAJIMA, Sachiko
; APPLICANT: KURANO, Yoshihiro
; APPLICANT: NAKATSUBO, Kaoru
; APPLICANT: NISHIZONO, Isao
; TITLE OF INVENTION: Immunoassay For Measuring Human C-Peptide and Kit
Therefor
; FILE REFERENCE: 0760-0291P
; CURRENT APPLICATION NUMBER: US/09/878,380
; CURRENT FILING DATE: 2001-06-12
; PRIOR APPLICATION NUMBER: JP 2000-174691
; PRIOR FILING DATE: 2000-06-12
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-878-380-1
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Query Match          100.0%; Score 463; DB 9; Length 86;
Best Local Similarity 100.0%; Pred. No. 1.3e-44;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60
          |||
Db      1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60

Qy      61 SLQKRGIVEQCCTSICSLYQLENYCN 86
          |||
Db      61 SLQKRGIVEQCCTSICSLYQLENYCN 86
```

RESULT 2

US-09-858-935B-4

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; Sequence 4, Application US/09858935B
; Publication No. US20030069177A1
; GENERAL INFORMATION:
; APPLICANT: Dubaquier, Yves
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Lowman, Henry B.
; TITLE OF INVENTION: METHOD FOR TREATING CARTILAGE DISORDERS
; FILE REFERENCE: P1794R1
; CURRENT APPLICATION NUMBER: US/09/858,935B
; CURRENT FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: US 60/248,985
; PRIOR FILING DATE: 2000-11-15
; PRIOR APPLICATION NUMBER: US 60/204,490
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 153
; SEQ ID NO 4
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-858-935B-4
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Query Match 100.0%; Score 463; DB 10; Length 86;
Best Local Similarity 100.0%; Pred. No. 1.3e-44;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60
          |||
Db      1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60

Qy      61 SLQKRGIVEQCCTSICSLYQLENYCN 86
          |||
Db      61 SLQKRGIVEQCCTSICSLYQLENYCN 86
```

RESULT 3

US-10-028-410-2
; Sequence 2, Application US/10028410
; Publication No. US20020160955A1
; GENERAL INFORMATION:
; APPLICANT: Dubaquie, Yves
; APPLICANT: Lowman, Henry
; TITLE OF INVENTION: PROTEIN VARIANTS
; FILE REFERENCE: P1712R1-1
; CURRENT APPLICATION NUMBER: US/10/028,410
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: US/09/477,924
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 6
; SEQ ID NO 2
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-028-410-2

Query Match 100.0%; Score 463; DB 13; Length 86;
Best Local Similarity 100.0%; Pred. No. 1.3e-44;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60
          |||
Db      1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60

Qy      61 SLQKRGIVEQCCTSICSLYQLENYCN 86
          |||
Db      61 SLQKRGIVEQCCTSICSLYQLENYCN 86
```

RESULT 4

US-10-054-873-4
; Sequence 4, Application US/10054873
; Publication No. US20020164712A1
; GENERAL INFORMATION:
; APPLICANT: Gan, Zhong Ru
; TITLE OF INVENTION: Chimeric Protein Containing an
; Intramolecular Chaperone-Like Sequence
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP

```

; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/054,873
; FILING DATE: 22-Jan-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/CN98/00052
; FILING DATE: 31-MAR-1998
; APPLICATION NUMBER: US 09/423,100
; FILING DATE: 11-DEC-2000
; ATTORNEY/AGENT INFORMATION:
; NAME: Mycroft, Frank J
; REGISTRATION NUMBER: 46,946
; REFERENCE/DOCKET NUMBER: 020167-000130US
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 86 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-054-873-4

```

```

Query Match          100.0%;  Score 463;  DB 13;  Length 86;
Best Local Similarity 100.0%;  Pred. No. 1.3e-44;
Matches    86;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

```

```

Qy      1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60
        |||
Db      1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60

Qy      61 SLQKRGIVEQCCTSICSLYQLENYCN 86
        |||
Db      61 SLQKRGIVEQCCTSICSLYQLENYCN 86

```

```

RESULT 5
US-10-444-326-2
; Sequence 2, Application US/10444326
; Publication No. US20030191065A1
; GENERAL INFORMATION:
; APPLICANT: Dubaquie, Yves
; APPLICANT: Lowman, Henry
; TITLE OF INVENTION: PROTEIN VARIANTS
; FILE REFERENCE: P1712R1
; CURRENT APPLICATION NUMBER: US/10/444,326
; CURRENT FILING DATE: 2003-05-22

```

; PRIOR APPLICATION NUMBER: US/09/723,866
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US/09/477,923
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 6
; SEQ ID NO 2
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-444-326-2

Query Match 100.0%; Score 463; DB 14; Length 86;
Best Local Similarity 100.0%; Pred. No. 1.3e-44;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPIALEG 60
|
Db 1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPIALEG 60

Qy 61 SLQKRGIVEQCCTSICSLYQLENYCN 86
|
Db 61 SLQKRGIVEQCCTSICSLYQLENYCN 86

RESULT 6

US-10-271-869-4

; Sequence 4, Application US/10271869
; Publication No. US20030211992A1
; GENERAL INFORMATION:
; APPLICANT: Dubaquie, Yves
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Lowman, Henry B.
; TITLE OF INVENTION: METHOD FOR TREATING CARTILAGE DISORDERS
; FILE REFERENCE: P1794R1
; CURRENT APPLICATION NUMBER: US/10/271,869
; CURRENT FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: US/09/858,935
; PRIOR FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: US 60/248,985
; PRIOR FILING DATE: 2000-11-15
; PRIOR APPLICATION NUMBER: US 60/204,490
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 153
; SEQ ID NO 4
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-271-869-4

Query Match 100.0%; Score 463; DB 15; Length 86;
Best Local Similarity 100.0%; Pred. No. 1.3e-44;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPIALEG 60
|
Db 1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPIALEG 60

Qy 61 SLQKRGIVEQCCTSICSLYQLENYCN 86
|||||
Db 61 SLQKRGIVEQCCTSICSLYQLENYCN 86

RESULT 7

US-10-444-262-2
; Sequence 2, Application US/10444262
; Publication No. US20040023883A1
; GENERAL INFORMATION:
; APPLICANT: Dubaquier, Yves
; APPLICANT: Lowman, Henry
; TITLE OF INVENTION: PROTEIN VARIANTS
; FILE REFERENCE: P1712R1
; CURRENT APPLICATION NUMBER: US/10/444,262
; CURRENT FILING DATE: 2003-05-22
; PRIOR APPLICATION NUMBER: US/09/724,478
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US/09/477,923
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 6
; SEQ ID NO 2
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-444-262-2

Query Match 100.0%; Score 463; DB 15; Length 86;
Best Local Similarity 100.0%; Pred. No. 1.3e-44;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60
|||||
Db 1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60

Qy 61 SLQKRGIVEQCCTSICSLYQLENYCN 86
|||||
Db 61 SLQKRGIVEQCCTSICSLYQLENYCN 86

RESULT 8

US-10-444-649-2
; Sequence 2, Application US/10444649
; Publication No. US20040033951A1
; GENERAL INFORMATION:
; APPLICANT: Dubaquier, Yves
; APPLICANT: Lowman, Henry
; TITLE OF INVENTION: PROTEIN VARIANTS
; FILE REFERENCE: P1712R1
; CURRENT APPLICATION NUMBER: US/10/444,649
; CURRENT FILING DATE: 2003-05-22
; PRIOR APPLICATION NUMBER: US/09/724,479
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US/09/477,923
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 6
; SEQ ID NO 2

; LENGTH: 86
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-444-649-2

Query Match 100.0%; Score 463; DB 15; Length 86;
Best Local Similarity 100.0%; Pred. No. 1.3e-44;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60
|
Db 1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60

Qy 61 SLQKRGIVEQCCTSICSLYQLENYCN 86
|
Db 61 SLQKRGIVEQCCTSICSLYQLENYCN 86

RESULT 9

US-10-444-701-2
; Sequence 2, Application US/10444701
; Publication No. US20040033952A1
; GENERAL INFORMATION:
; APPLICANT: Dubaquier, Yves
; APPLICANT: Lowman, Henry
; TITLE OF INVENTION: PROTEIN VARIANTS
; FILE REFERENCE: P1712R1
; CURRENT APPLICATION NUMBER: US/10/444,701
; CURRENT FILING DATE: 2003-05-22
; PRIOR APPLICATION NUMBER: US/09/723,866
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US/09/477,923
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 6
; SEQ ID NO 2
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-444-701-2

Query Match 100.0%; Score 463; DB 15; Length 86;
Best Local Similarity 100.0%; Pred. No. 1.3e-44;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60
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Db 1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60

Qy 61 SLQKRGIVEQCCTSICSLYQLENYCN 86
|
Db 61 SLQKRGIVEQCCTSICSLYQLENYCN 86

RESULT 10

US-10-760-928-2
; Sequence 2, Application US/10760928
; Publication No. US20050026826A1

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; GENERAL INFORMATION:
; APPLICANT: HOENIG, MARGARETHE
; TITLE OF INVENTION: FELINE PROINSULIN, INSULIN AND CONSTITUENT PEPTIDES
; FILE REFERENCE: 235.00520101
; CURRENT APPLICATION NUMBER: US/10/760,928
; CURRENT FILING DATE: 2004-01-20
; PRIOR APPLICATION NUMBER: 60/440,964
; PRIOR FILING DATE: 2003-01-17
; PRIOR APPLICATION NUMBER: 60/444,009
; PRIOR FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 2
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-760-928-2
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Query Match          100.0%; Score 463; DB 17; Length 86;
Best Local Similarity 100.0%; Pred. No. 1.3e-44;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60
          |||
Db      1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60

Qy      61 SLQKRGIVEQCCTSICSLYQLENYCN 86
          |||
Db      61 SLQKRGIVEQCCTSICSLYQLENYCN 86
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RESULT 11

```
US-10-869-040-89
; Sequence 89, Application US/10869040
; Publication No. US20050039235A1
; GENERAL INFORMATION:
; APPLICANT: Moloney, Maurice M.
; APPLICANT: Boothe, Joseph
; APPLICANT: Keon, Richard
; APPLICANT: Nykiforuk, Cory
; APPLICANT: Van Rooijen, Gijs
; TITLE OF INVENTION: Methods for the Production of Insulin in Plants
; FILE REFERENCE: 9369-301
; CURRENT APPLICATION NUMBER: US/10/869,040
; CURRENT FILING DATE: 2004-06-17
; PRIOR APPLICATION NUMBER: 60/478,818
; PRIOR FILING DATE: 2003-06-17
; PRIOR APPLICATION NUMBER: 60/549,539
; PRIOR FILING DATE: 2004-03-04
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 89
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Proinsulin
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Query Match          100.0%; Score 463; DB 17; Length 87;
Best Local Similarity 100.0%; Pred. No. 1.3e-44;
Matches      86; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

Qy      1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60
        |||
Db      2 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 61

Qy      61 SLQKRGIVEQCCTSICSLYQLENYCN 86
        |||
Db      62 SLQKRGIVEQCCTSICSLYQLENYCN 87

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US-09-947-563-4
; Sequence 4, Application US/09947563
; Patent No. US20020156234A1
;   GENERAL INFORMATION:
;       APPLICANT: Rubroder, Franz-Josef
;               Keller, Reinhold
;       TITLE OF INVENTION: Improved process for obtaining
;                           insulin precursors having correctly bonded cystine
bridges
;       NUMBER OF SEQUENCES: 7
;       CORRESPONDENCE ADDRESS:
;           ADDRESSEE: Finnegan, Henderson, Farrabow, Garrett &
;                   Dunner
;           STREET: 1300 I Street, N.W.
;           CITY: Washington
;           STATE: D.C.
;           COUNTRY: USA
;           ZIP: 20005-3315
;       COMPUTER READABLE FORM:
;           MEDIUM TYPE: Floppy disk
;           COMPUTER: IBM PC compatible
;           OPERATING SYSTEM: PC-DOS/MS-DOS
;           SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;           APPLICATION NUMBER: US/09/947,563
;           FILING DATE: 07-Sep-2001
;           CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;           APPLICATION NUMBER: 09/134,836
;           FILING DATE: <Unknown>
;       ATTORNEY/AGENT INFORMATION:
;           NAME: Leslie McDonell
;           REGISTRATION NUMBER: 34,872
;           REFERENCE/DOCKET NUMBER: 02481.1600-00000
;       TELECOMMUNICATION INFORMATION:
;           TELEPHONE: (202) 408-4000
;           TELEFAX: (202) 408-4400
;       INFORMATION FOR SEQ ID NO: 4:
;           SEQUENCE CHARACTERISTICS:
;               LENGTH: 96 amino acids
;               TYPE: amino acid

```

```

;          STRANDEDNESS: single
;          TOPOLOGY: linear
;          MOLECULE TYPE: protein
;          ORIGINAL SOURCE:
;          ORGANISM: Escherichia coli
;          FEATURE:
;          NAME/KEY: Protein
;          LOCATION: 1..96
;          SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-947-563-4

```

```

Query Match          100.0%;  Score 463;  DB 9;  Length 96;
Best Local Similarity 100.0%;  Pred. No. 1.5e-44;
Matches    86;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

```

```

Qy          1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60
            |||
Db          11 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 70

Qy          61 SLQKRGIVEQCCTSICSLYQLENYCN 86
            |||
Db          71 SLQKRGIVEQCCTSICSLYQLENYCN 96

```

RESULT 13

US-09-205-658-125

```

; Sequence 125, Application US/09205658
; Patent No. US20010029617A1
; GENERAL INFORMATION:
; APPLICANT: Ruvkun, Gary
; APPLICANT: Ogg, Scott
; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR
; TITLE OF INVENTION: IMPAIRED GLUCOSE TOLERANCE CONDITIONS
; FILE REFERENCE: 00786/351004
; CURRENT APPLICATION NUMBER: US/09/205,658
; CURRENT FILING DATE: 1998-12-03
; EARLIER APPLICATION NUMBER: 08/857,076
; EARLIER FILING DATE: 1997-05-15
; EARLIER APPLICATION NUMBER: 08/888,534
; EARLIER FILING DATE: 1997-07-07
; EARLIER APPLICATION NUMBER: US98/10080
; EARLIER FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 328
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 125
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-205-658-125

```

```

Query Match          100.0%;  Score 463;  DB 9;  Length 110;
Best Local Similarity 100.0%;  Pred. No. 1.8e-44;
Matches    86;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

```

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Qy          1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60
            |||
Db          25 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 84

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RESULT 15
US-09-804-409A-9
; Sequence 9, Application US/09804409A
; Patent No. US20020155100A1
; GENERAL INFORMATION:
; APPLICANT: KIEFFER, TIMOTHY J.
; APPLICANT: CHEUNG, ANTHONY T.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR REGULATED PROTEIN
; TITLE OF INVENTION: EXPRESSION IN GUT
; FILE REFERENCE: 029996/027 8721
; CURRENT APPLICATION NUMBER: US/09/804,409A
; CURRENT FILING DATE: 2001-03-12
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 110
; TYPE: PRT

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; ORGANISM: Homo sapiens
US-09-804-409A-9

Query Match 100.0%; Score 463; DB 9; Length 110;
Best Local Similarity 100.0%; Pred. No. 1.8e-44;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      25 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 84

Qy      61 SLQKRGIVEQCCTSICSLYQLENYCN 86
          ||||||||||||||||||||
Db      85 SLQKRGIVEQCCTSICSLYQLENYCN 110
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Search completed: March 9, 2005, 05:12:20
Job time : 181.996 secs

OM protein - protein search, using sw model

Run on: March 9, 2005, 01:51:53 ; Search time 16.5018 Seconds
(without alignments)
501.437 Million cell updates/sec

Title: US-10-054-873-4
Perfect score: 463
Sequence: 1 FVNQHLCGSHLVEALYLVCG.....IVEQCCTSICSLYQLENYCN 86

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query				Description
		Match	Length	DB	ID	
1	463	100.0	110	1	IPHU	insulin precursor
2	463	100.0	110	2	A42179	insulin precursor
3	456	98.5	110	2	B42179	insulin precursor
4	456	98.5	110	2	JQ0178	insulin precursor
5	424	91.6	110	1	INRB	insulin precursor
6	417	90.1	110	1	IPDG	insulin precursor
7	394	85.1	86	1	IPHO	insulin precursor
8	394	85.1	110	1	INMS2	insulin 2 precursor
9	394	85.1	110	1	IPRT2	insulin 2 precursor
10	392	84.7	108	2	A39883	insulin precursor
11	392	84.7	110	2	I48166	insulin precursor
12	385	83.2	110	1	IPRT1	insulin 1 precursor
13	383	82.7	84	1	IPPG	insulin precursor

14	366.5	79.2	105	1	IPBO	insulin precursor
15	366	79.0	108	1	INMS1	insulin 1 precurs
16	334.5	72.2	108	2	S09278	insulin precursor
17	320.5	69.2	77	1	INSH	insulin precursor
18	314	67.8	110	1	IPGP	insulin precursor
19	277.5	59.9	109	1	IPRTDU	insulin precursor
20	276.5	59.7	103	2	I51221	insulin precursor
21	265.5	57.3	106	1	IPXL2	insulin II precurs
22	265.5	57.3	107	1	IPCH	insulin precursor
23	262.5	56.7	106	1	IPXL1	insulin I precurs
24	256.5	55.4	51	1	INEL	insulin - elephant
25	256.5	55.4	51	1	INWHF	insulin - finback
26	256.5	55.4	51	1	INWHP	insulin - sperm wh
27	256.5	55.4	81	1	IPDK	insulin precursor
28	256	55.3	96	2	PC7082	epidermal growth f
29	254.5	55.0	51	1	INHY	insulin - hamster
30	251.5	54.3	51	1	INMSSP	insulin - Egyptian
31	250.5	54.1	51	2	A59151	insulin precursor
32	246.5	53.2	51	1	INCMA	insulin - Arabian
33	246.5	53.2	51	1	INGT	insulin - goat
34	246.5	53.2	51	1	INWH1S	insulin - sei whal
35	245.5	53.0	51	1	INCT	insulin - cat
36	244.5	52.8	51	1	INMKSQ	insulin - common s
37	239.5	51.7	51	2	JQ0362	insulin - North Am
38	234.5	50.6	51	1	INCB	insulin - Chinchil
39	231.5	50.0	51	1	INGS	insulin - goose
40	227.5	49.1	51	1	INOS	insulin - ostrich
41	227.5	49.1	51	1	INTK	insulin - turkey (
42	227.5	49.1	51	1	A61129	insulin - black-be
43	227.5	49.1	51	1	INPQ	insulin - crested
44	227.5	49.1	51	2	A60414	insulin - slider t
45	225	48.6	52	2	S44470	insulin I2 - North

ALIGNMENTS

RESULT 1

IPHU

insulin precursor [validated] - human

N;Alternate names: preproinsulin

C;Species: Homo sapiens (man)

C;Date: 23-Oct-1981 #sequence_revision 23-Oct-1981 #text_change 09-Jul-2004

C;Accession: A93222; A94253; A93216; A94251; A93144; A92075; A91186; I58114; A01579; S58661

R;Bell, G.I.; Pictet, R.L.; Rutter, W.J.; Cordell, B.; Tischer, E.; Goodman, H.M.

Nature 284, 26-32, 1980

A;Title: Sequence of the human insulin gene.

A;Reference number: A93222; MUID:80120725; PMID:6243748

A;Accession: A93222

A;Molecule type: DNA

A;Residues: 1-110 <BEL>

A;Cross-references: UNIPROT:P01308; GB:J00265; NID:g186429; PIDN:AAA59172.1; PID:g386828

R;Ullrich, A.; Dull, T.J.; Gray, A.; Brosius, J.; Sures, I.

Science 209, 612-615, 1980

A;Title: Genetic variation in the human insulin gene.
 A;Reference number: A94253; MUID:80236313; PMID:6248962
 A;Accession: A94253
 A;Molecule type: DNA
 A;Residues: 1-110 <ULL>
 A;Cross-references: GB:J00265; NID:g186429; PIDN:AAA59172.1; PID:g386828
 R;Bell, G.I.; Swain, W.F.; Pictet, R.; Cordell, B.; Goodman, H.M.; Rutter, W.J.
 Nature 282, 525-527, 1979
 A;Title: Nucleotide sequence of a cDNA clone encoding human preproinsulin.
 A;Reference number: A93216; MUID:80054779; PMID:503234
 A;Accession: A93216
 A;Molecule type: mRNA
 A;Residues: 1-110 <BEL2>
 A;Cross-references: GB:J00265; NID:g186429; PIDN:AAA59172.1; PID:g386828
 R;Sures, I.; Goeddel, D.V.; Gray, A.; Ullrich, A.
 Science 208, 57-59, 1980
 A;Title: Nucleotide sequence of human preproinsulin complementary DNA.
 A;Reference number: A94251; MUID:80147417; PMID:6927840
 A;Accession: A94251
 A;Molecule type: mRNA
 A;Residues: 1-110 <SUR>
 A;Cross-references: GB:J00265; NID:g186429; PIDN:AAA59172.1; PID:g386828
 R;Nicol, D.S.H.W.; Smith, L.F.
 Nature 187, 483-485, 1960
 A;Title: Amino-acid sequence of human insulin.
 A;Reference number: A93144
 A;Accession: A93144
 A;Molecule type: protein
 A;Residues: 25-54;90-110 <NIC>
 R;Oyer, P.E.; Cho, S.; Peterson, J.D.; Steiner, D.F.
 J. Biol. Chem. 246, 1375-1386, 1971
 A;Title: Studies on human proinsulin. Isolation and amino acid sequence of the human pancreatic C-peptide.
 A;Reference number: A92075; MUID:71116410; PMID:5101771
 A;Accession: A92075
 A;Molecule type: protein
 A;Residues: 57-87 <OYE>
 R;Ko, A.; Smyth, D.G.; Markussen, J.; Sundby, F.
 Eur. J. Biochem. 20, 190-199, 1971
 A;Title: Amino acid sequence of the C-peptide of human proinsulin.
 A;Reference number: A91186; MUID:71257722; PMID:5560404
 A;Accession: A91186
 A;Molecule type: protein
 A;Residues: 57-87 <KOA>
 R;Lucassen, A.M.; Julier, C.; Beressi, J.P.; Boitard, C.; Froguel, P.; Lathrop, M.; Bell, J.I.
 Nature Genet. 4, 305-310, 1993
 A;Title: Susceptibility to insulin dependent diabetes mellitus maps to a 4.1 kb segment of DNA spanning the insulin gene and associated VNTR.
 A;Reference number: I58114; MUID:93364428; PMID:8358440
 A;Accession: I58114
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-59,63-110 <RES>
 A;Cross-references: GB:L15440; NID:g307071; PIDN:AAA59179.1; PID:g307072
 R;Sieber, P.; Kamber, B.; Hartmann, A.; Joehl, A.; Riniker, B.; Rittel, W.
 Helv. Chim. Acta 57, 2617-2621, 1974

A;Title: Totalsynthese von Humaninsulin unter gezielter Bildung der Disulfidbindungen.
A;Reference number: A91636; MUID:75077277; PMID:4443293
A;Contents: annotation; synthesis
A;Note: disulfide-bonded human insulin was synthesized; the synthetic hormone was identical with the natural hormone in chemical and biological activities
A;Note: article in German with English abstract
R;Naithani, V.K.
Hoppe-Seyler's Z. Physiol. Chem. 354, 659-672, 1973
A;Title: The synthesis of C-peptide of human proinsulin.
A;Reference number: A91658; MUID:75040007; PMID:4803504
A;Contents: annotation; synthesis of residues 57-87
R;Geiger, R.; Jaeger, G.; Koenig, W.
Chem. Ber. 106, 2347-2352, 1973
A;Title: Synthesis of the complete sequence of human proinsulin C-peptide and its [Glu-9,Gln-11] analogue.
A;Reference number: A90914
A;Contents: annotation; synthesis of residues 57-87
R;Kaufmann, J.E.; Irminger, J.C.; Halban, P.A.
Biochem. J. 310, 869-874, 1995
A;Title: Sequence requirements for proinsulin processing at the B-chain/C-peptide junction.
A;Reference number: S58661; MUID:96013185; PMID:7575420
A;Contents: annotation; site-directed mutagenesis study of proteolytic processing
C;Genetics:
A;Gene: GDB:INS
A;Cross-references: GDB:119349; OMIM:176730
A;Map position: 11p15.5-11p15.5
A;Introns: 63/1
C;Superfamily: insulin
C;Keywords: hormone; pancreas
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-54/Domain: insulin chain B #status experimental <BCH>
F;25-54,90-110/Product: insulin #status experimental <MAT>
F;57-87/Domain: connecting C peptide #status experimental <CPEP>
F;90-110/Domain: insulin chain A #status experimental <ACH>
F;31-96,43-109,95-100/Disulfide bonds: #status experimental

Query Match 100.0%; Score 463; DB 1; Length 110;
Best Local Similarity 100.0%; Pred. No. 6.8e-43;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60
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Db      25 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 84

Qy      61 SLQKRGIVEQCCTSICSLYQLENYCN 86
          |||
Db      85 SLQKRGIVEQCCTSICSLYQLENYCN 110

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RESULT 2
A42179
insulin precursor - chimpanzee
C;Species: Pan troglodytes (chimpanzee)
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004

C;Accession: A42179; S22058
 R;Seino, S.; Bell, G.I.; Li, W.H.
 Mol. Biol. Evol. 9, 193-203, 1992
 A;Title: Sequences of primate insulin genes support the hypothesis of a slower rate of molecular evolution in humans and apes than in monkeys.
 A;Reference number: A42179; MUID:92219953; PMID:1560757
 A;Accession: A42179
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-110 <SEI>
 A;Cross-references: UNIPROT:P30410; EMBL:X61089; NID:g38251; PIDN:CAA43403.1; PID:g38252
 A;Note: sequence extracted from NCBI backbone (NCBIP:95067)
 C;Genetics:
 A;Introns: 63/1
 C;Superfamily: insulin

Query Match 100.0%; Score 463; DB 2; Length 110;
 Best Local Similarity 100.0%; Pred. No. 6.8e-43;
 Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60
          |||
Db      25 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 84

Qy      61 SLQKRGIVEQCCTSICSLYQLENYCN 86
          |||
Db      85 SLQKRGIVEQCCTSICSLYQLENYCN 110
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RESULT 3

B42179

insulin precursor - green monkey

C;Species: Cercopithecus aethiops (green monkey, grivet)

C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004

C;Accession: B42179; A05232; S16494; S22056

R;Seino, S.; Bell, G.I.; Li, W.H.

Mol. Biol. Evol. 9, 193-203, 1992

A;Title: Sequences of primate insulin genes support the hypothesis of a slower rate of molecular evolution in humans and apes than in monkeys.

A;Reference number: A42179; MUID:92219953; PMID:1560757

A;Accession: B42179

A;Molecule type: DNA

A;Residues: 1-110 <SEI>

A;Cross-references: UNIPROT:P30407; EMBL:X61092; NID:g22808; PIDN:CAA43405.1; PID:g22809

A;Note: sequence extracted from NCBI backbone (NCBIN:95185, NCBIP:95194)

R;Peterson, J.D.; Nehrlich, S.; Oyer, P.E.; Steiner, D.F.

J. Biol. Chem. 247, 4866-4871, 1972

A;Title: Determination of the amino acid sequence of the monkey, sheep, and dog proinsulin C-peptides by a semi-micro Edman degradation procedure.

A;Reference number: A92111; MUID:72258016; PMID:4626369

A;Accession: A05232

A;Molecule type: protein

A;Residues: 57-87 <PET>

C;Genetics:

A;Introns: 63/1

C;Superfamily: insulin
C;Keywords: hormone; pancreas
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-54/Domain: insulin chain B #status predicted <BCH>
F;25-54,90-110/Product: insulin #status predicted <MAT>
F;57-87/Domain: connecting peptide #status experimental <CPEP>
F;90-110/Domain: insulin chain A #status predicted <ACH>
F;31-96,43-109,95-100/Disulfide bonds: #status predicted

Query Match 98.5%; Score 456; DB 2; Length 110;
Best Local Similarity 98.8%; Pred. No. 3.9e-42;
Matches 85; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db      25 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDPQVGQVELGGGPGAGSLQPLALEG 84

Qy      61 SLQKRGIVEQCCTSICSLYQLENYCN 86
          ||||||||||||||||||||||||||||
Db      85 SLQKRGIVEQCCTSICSLYQLENYCN 110
```

RESULT 4

JQ0178

insulin precursor - crab-eating macaque

C;Species: *Macaca fascicularis* (crab-eating macaque)

C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004

C;Accession: JQ0178

R;Wetekam, W.; Groneberg, J.; Leineweber, M.; Wengenmayer, F.; Winnacker, E.L.
Gene 19, 179-183, 1982

A;Title: The nucleotide sequence of cDNA coding for preproinsulin from the
primate *Macaca fascicularis*.

A;Reference number: JQ0178; MUID:83080474; PMID:6184262

A;Accession: JQ0178

A;Molecule type: mRNA

A;Residues: 1-110 <WET>

A;Cross-references: UNIPROT:P30406; GB:J00336; NID:g342121; PIDN:AAA36849.1;
PID:g342122

C;Superfamily: insulin

F;1-24/Domain: signal sequence #status predicted <SIG>

F;25-54,90-110/Product: insulin #status predicted <MAT>

F;25-54/Domain: insulin chain B #status predicted <BCH>

F;55-89/Domain: insulin connecting C peptide #status predicted <CPT>

F;90-110/Domain: insulin chain A #status predicted <ACH>

F;31-96,43-109,95-100/Disulfide bonds: #status predicted

Query Match 98.5%; Score 456; DB 2; Length 110;
Best Local Similarity 98.8%; Pred. No. 3.9e-42;
Matches 85; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60
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Db      25 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDPQVGQVELGGGPGAGSLQPLALEG 84

Qy      61 SLQKRGIVEQCCTSICSLYQLENYCN 86
          ||||||||||||||||||||||||||||
Db      85 SLQKRGIVEQCCTSICSLYQLENYCN 110
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A;Title: Cloning and nucleotide sequence analysis of the dog insulin gene. Coded amino acid sequence of canine preproinsulin predicts an additional C-peptide fragment.

A;Accession: A92413

A;Residues: 1-110 <SMI>

PIDN:CAA23475.1; PID:g995

Am. J. Med. 40, 662-666, 1966

A;Reference number: A90029; MUID:66160119; PMID:5949593

A;Molecule type: protein

R; Peterson, J.D.; Nehrlich, S.; Oyer, P.E.; Steiner, D.F.

A;Title: Determination of the amino acid sequence of the monkey, sheep, and dog proinsulin C-peptides by a semi-micro Edman degradation procedure.

A;Accession: S16493

A;Residues: 65-85, 'I', 87 <PET>

C;Keywords: hormone; pancreas

F;25-54/Domain: insulin chain B #status experimental <BCH>

F;57-87/Domain: connecting peptide #status predicted <CPEP>

F;31-96,43-109,95-100/Disulfide bonds: #status experimental

Best Local Similarity 89.5%; Pred. No. 6.3e-38;

Db 25 FVNQHLCGSHLVEALYLVCGERGFFYTPKARREVEDLQVRDVELAGAPGEGGLOPLALEG 84

: | | | | | | | | | | | | | | | | | | | | |

Db 85 ALQKRGIVEQCCTSI CSLYQLENYCN 110

IPHO

C;Species: Equus caballus (domestic horse)

C;Accession: A01580; A92120

Arch. Biochem. Biophys. 65, 427-428, 1956

A;Reference number: A90082

A;Accession: A01580
 A;Molecule type: protein
 A;Residues: 1-30;66-86 <HAR>
 A;Cross-references: UNIPROT:P01310
 R;Tager, H.S.; Steiner, D.F.
 J. Biol. Chem. 247, 7936-7940, 1972
 A;Title: Primary structures of the proinsulin connecting peptides of the rat and horse.
 A;Reference number: A92120; MUID:73061498; PMID:4640931
 A;Accession: A92120
 A;Molecule type: protein
 A;Residues: 33-63 <TAG>
 C;Comment: X's at positions 31-32 and 64-65 represent paired basic residues assumed (by homology) to be present in the precursor molecule.
 C;Superfamily: insulin
 C;Keywords: hormone; pancreas
 F;1-30/Domain: insulin chain B #status experimental <BCH>
 F;1-30,66-86/Product: insulin #status experimental <MAT>
 F;33-63/Domain: connecting peptide #status experimental <CPEP>
 F;66-86/Domain: insulin chain A #status experimental <ACH>
 F;7-72,19-85,71-76/Disulfide bonds: #status predicted

Query Match 85.1%; Score 394; DB 1; Length 86;
 Best Local Similarity 84.9%; Pred. No. 1.5e-35;
 Matches 73; Conservative 1; Mismatches 12; Indels 0; Gaps 0;

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Qy      1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60
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Db      1 FVNQHLCGSHLVEALYLVCGERGFFYTPKAXXEAEDPQVGEVELGGGPGGLQPLALAG 60

Qy      61 SLQKRGIVEQCCTSICSLYQLENYCN 86
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Db      61 PQQXXGIVEQCCTGICSLYQLENYCN 86
  
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RESULT 8

INMS2

insulin 2 precursor - mouse

C;Species: Mus musculus (house mouse)

C;Date: 31-Mar-1992 #sequence_revision 14-Jul-1994 #text_change 09-Jul-2004

C;Accession: A26342; B48172; A61012; B01592

R;Wentworth, B.M.; Schaefer, I.M.; Villa-Komaroff, L.; Chirgwin, J.M.

J. Mol. Evol. 23, 305-312, 1986

A;Title: Characterization of the two nonallelic genes encoding mouse preproinsulin.

A;Reference number: A92965; MUID:87169768; PMID:3104603

A;Accession: A26342

A;Molecule type: DNA

A;Residues: 1-110 <WEN>

A;Cross-references: UNIPROT:P01326; GB:X04724; NID:g52714; PIDN:CAA28433.1; PID:g52715

R;Sawa, T.; Ohgaku, S.; Morioka, H.; Yano, S.

J. Mol. Endocrinol. 5, 61-67, 1990

A;Title: Molecular cloning and DNA sequence analysis of preproinsulin genes in the NON mouse, an animal model of human non-obese, non-insulin-dependent diabetes mellitus.

A;Reference number: A48172; MUID:90372989; PMID:2397023

A;Residues: 1-110 <LOM>
A;Cross-references: UNIPROT:P01323; GB:J00748; NID:g204958; PIDN:AAA41443.1; PID:g204959
R;Steiner, D.F.; Clark, J.L.; Nolan, C.; Rubenstein, A.H.; Margoliash, E.; Aten, B.; Oyer, P.E.
Recent Prog. Horm. Res. 25, 207-282, 1969
A;Title: Proinsulin and the biosynthesis of insulin.
A;Reference number: A94231; MUID:70067613; PMID:4311938
A;Accession: B94231
A;Molecule type: protein
A;Residues: 25-54;90-110 <STE>
R;Tager, H.S.; Steiner, D.F.
J. Biol. Chem. 247, 7936-7940, 1972
A;Title: Primary structures of the proinsulin connecting peptides of the rat and horse.
A;Reference number: A92120; MUID:73061498; PMID:4640931
A;Accession: C92120
A;Molecule type: protein
A;Residues: 57-87 <TAG>
R;Lomedico, P.T.; Rosenthal, N.; Kolodner, R.; Efstratiadis, A.; Gilbert, W.
Ann. N. Y. Acad. Sci. 343, 425-432, 1980
A;Title: The structure of rat preproinsulin genes.
A;Reference number: I51945; MUID:80240379; PMID:6249167
A;Accession: I64880
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-110 <RES>
A;Cross-references: GB:M25585; NID:g204950; PIDN:AAA41440.1; PID:g204952
C;Genetics:
A;Gene: INS2
A;Introns: 63/1
C;Superfamily: insulin
C;Keywords: hormone; pancreas
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-54/Domain: insulin chain B #status experimental <BCH>
F;25-54,90-110/Product: insulin #status experimental <MAT>
F;57-87/Domain: connecting peptide #status experimental <CPEP>
F;90-110/Domain: insulin chain A #status experimental <ACH>
F;31-96,43-109,95-100/Disulfide bonds: #status experimental

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Matches 73; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

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Db      25 FVKQHLCGSHLVEALYLVCGERGFFYTPMSRREVEDPQVAQLQLGGGPGAGDLQTLALEV 84

Qy      61 SLQKRGIVEQCCTSICSLYQLENYCN 86
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Db      85 ARQKRGIVDQCCTSICSLYQLENYCN 110
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RESULT 10

A39883

insulin precursor - douroucouli

C;Species: Aotus trivirgatus (douroucouli, night monkey, owl monkey)

RESULT 12

IPRT1

insulin 1 precursor - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 23-Oct-1981 #sequence_revision 23-Oct-1981 #text_change 09-Jul-2004

C;Accession: A90788; A90789; A94231; B92120; I51945; A01589

R;Cordell, B.; Bell, G.; Tischer, E.; DeNoto, F.M.; Ullrich, A.; Pictet, R.; Rutter, W.J.; Goodman, H.M.

Cell 18, 533-543, 1979

A;Title: Isolation and characterization of a cloned rat insulin gene.

A;Reference number: A90788; MUID:80045034; PMID:498283

A;Accession: A90788

A;Molecule type: DNA

A;Residues: 1-110 <COR>

A;Cross-references: UNIPROT:P01322; GB:J00747; NID:g204956; PIDN:AAA41442.1; PID:g204957

R;Lomedico, P.; Rosenthal, N.; Efstratiadis, A.; Gilbert, W.; Kolodner, R.; Tizard, R.

Cell 18, 545-558, 1979

A;Title: The structure and evolution of the two nonallelic rat preproinsulin genes.

A;Reference number: A90789; MUID:80045035; PMID:498284

A;Accession: A90789

A;Molecule type: DNA

A;Residues: 1-110 <LOM>

A;Cross-references: GB:J00747; NID:g204956; PIDN:AAA41442.1; PID:g204957

R;Steiner, D.F.; Clark, J.L.; Nolan, C.; Rubenstein, A.H.; Margoliash, E.; Aten, B.; Oyer, P.E.

Recent Prog. Horm. Res. 25, 207-282, 1969

A;Title: Proinsulin and the biosynthesis of insulin.

A;Reference number: A94231; MUID:70067613; PMID:4311938

A;Accession: A94231

A;Molecule type: protein

A;Residues: 25-54;90-110 <STE>

R;Tager, H.S.; Steiner, D.F.

J. Biol. Chem. 247, 7936-7940, 1972

A;Title: Primary structures of the proinsulin connecting peptides of the rat and horse.

A;Reference number: A92120; MUID:73061498; PMID:4640931

A;Accession: B92120

A;Molecule type: protein

A;Residues: 57-87 <TAG>

R;Lomedico, P.T.; Rosenthal, N.; Kolodner, R.; Efstratiadis, A.; Gilbert, W. Ann. N. Y. Acad. Sci. 343, 425-432, 1980

A;Title: The structure of rat preproinsulin genes.

A;Reference number: I51945; MUID:80240379; PMID:6249167

A;Accession: I51945

A;Status: translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-110 <RES>

A;Cross-references: GB:M25584; NID:g204947; PIDN:AAA41439.1; PID:g204948

C;Genetics:

A;Gene: INS1

C;Superfamily: insulin

C;Keywords: hormone; pancreas

F;1-24/Domain: signal sequence #status predicted <SIG>

F;25-54/Domain: insulin chain B #status experimental <BCH>
F;25-54,90-110/Product: insulin #status experimental <MAT>
F;57-87/Domain: connecting peptide #status experimental <CPEP>
F;90-110/Domain: insulin chain A #status experimental <ACH>
F;31-96,43-109,95-100/Disulfide bonds: #status experimental

Query Match 83.2%; Score 385; DB 1; Length 110;
Best Local Similarity 83.7%; Pred. No. 1.8e-34;
Matches 72; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

Qy 1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60
|| ||||| |||||||||||||||||||:|||| || || |:||||| || || |||||
Db 25 FVKQHLCGPHLVEALYLVCGERGFFYTPKSRREVEDPQVPQLELGGGPEAGDLQTLALEV 84

Qy 61 SLQKRGIVEQCCTSICSLYQLENYCN 86
: |||||:|||||||||||||||
Db 85 ARQKRGIVDQCCTSICSLYQLENYCN 110

RESULT 13

IPPG

insulin precursor - pig

C;Species: Sus scrofa domestica (domestic pig)

C;Date: 22-Jun-1981 #sequence_revision 22-Jun-1981 #text_change 16-Jul-1999

C;Accession: A01583; A94572; S16492; A60835; B60835

R;Chance, R.E.; Ellis, R.M.; Bromer, W.W.

Science 161, 165-167, 1968

A;Title: Porcine proinsulin: characterization and amino acid sequence.

A;Reference number: A94240; MUID:68286485; PMID:5657063

A;Accession: A01583

A;Molecule type: protein

A;Residues: 1-34,'Q',36-84 <CHA>

R;Chance, R.E.

submitted to the Atlas, July 1970

A;Reference number: A94572

A;Accession: A94572

A;Molecule type: protein

A;Residues: 1-84 <CH2>

R;Brown, H.; Sanger, F.; Kitai, R.

Biochem. J. 60, 556-565, 1955

A;Title: The structure of pig and sheep insulins.

A;Reference number: A90344

A;Accession: S16492

A;Molecule type: protein

A;Residues: 1-30;31-51 <BRO>

R;Snel, L.; Damgaard, U.

Horm. Metab. Res. 20, 476-480, 1988

A;Title: Proinsulin heterogeneity in pigs.

A;Reference number: A60835; MUID:89032178; PMID:3181865

A;Accession: A60835

A;Molecule type: protein

A;Residues: 33-38,40-62 <SNE>

A;Note: the authors report the characterization of a connecting peptide variant lacking Ala-39

A;Accession: B60835

A;Molecule type: protein

A;Residues: 33-62 <SN2>

R;Blundell, T.; Dodson, G.; Hodgkin, D.; Mercola, D.
 Adv. Protein Chem. 26, 279-402, 1972
 A;Title: Insulin. the structure in the crystal and its reflection in chemistry and biology.
 A;Reference number: A90017
 A;Contents: annotation; X-ray crystallography, 1.9 angstroms
 C;Superfamily: insulin
 C;Keywords: hormone; pancreas
 F;1-30/Domain: insulin chain B #status experimental <BCH>
 F;1-30,64-84/Product: insulin #status experimental <MAT>
 F;33-63/Domain: connecting peptide #status experimental <CPEP>
 F;64-84/Domain: insulin chain A #status experimental <ACH>
 F;7-70,19-83,69-74/Disulfide bonds: #status experimental

Query Match 82.7%; Score 383; DB 1; Length 84;
 Best Local Similarity 86.0%; Pred. No. 2.3e-34;
 Matches 74; Conservative 1; Mismatches 9; Indels 2; Gaps 1;

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Qy      1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60
          |||||
Db      1 FVNQHLCGSHLVEALYLVCGERGFFYTPKARREAENPQAGAVELGG--GLGGQLQALALEG 58

Qy      61 SLQKRGIVEQCCTSICSLYQLENYCN 86
          |||||
Db      59 PPQKRGIVEQCCTSICSLYQLENYCN 84
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RESULT 14

IPBO

insulin precursor - bovine

C;Species: Bos primigenius taurus (cattle)

C;Date: 24-Apr-1984 #sequence_revision 22-Apr-1995 #text_change 09-Jul-2004

C;Accession: A40909; A92080; A92074; A91185; A90342; A90341; S48184; S48185; S46258; A01585

R;D'Agostino, J.; Younes, M.A.; White, J.W.; Besch, P.K.; Field, J.B.; Frazier, M.L.

Mol. Endocrinol. 1, 327-331, 1987

A;Title: Cloning and nucleotide sequence analysis of complementary deoxyribonucleic acid for bovine preproinsulin.

A;Reference number: A40909; MUID:88288209; PMID:2456452

A;Accession: A40909

A;Molecule type: mRNA

A;Residues: 1-105 <DAA>

A;Cross-references: UNIPROT:P01317; GB:M54979; NID:g163578; PIDN:AAA30722.1; PID:g163579

A;Experimental source: fetal pancreas

R;Nolan, C.; Margoliash, E.; Peterson, J.D.; Steiner, D.F.

J. Biol. Chem. 246, 2780-2795, 1971

A;Title: The structure of bovine proinsulin.

A;Reference number: A92080; MUID:71166442; PMID:4928892

A;Accession: A92080

A;Molecule type: protein

A;Residues: 25-105 <NOL>

R;Steiner, D.F.; Cho, S.; Oyer, P.E.; Terris, S.; Peterson, J.D.; Rubenstein, A.H.

J. Biol. Chem. 246, 1365-1374, 1971

A;Title: Isolation and characterization of proinsulin C-peptide from bovine pancreas.
 A;Reference number: A92074; MUID:71116409; PMID:5545080
 A;Accession: A92074
 A;Molecule type: protein
 A;Residues: 57-82 <STE>
 R;Salokangas, A.; Smyth, D.G.; Markussen, J.; Sundby, F.
 Eur. J. Biochem. 20, 183-189, 1971
 A;Title: Bovine proinsulin: amino acid sequence of the C-peptide isolated from pancreas.
 A;Reference number: A91185; MUID:71257721; PMID:5105368
 A;Accession: A91185
 A;Molecule type: protein
 A;Residues: 57-82 <SAL>
 R;Sanger, F.; Thompson, E.O.P.
 Biochem. J. 53, 366-374, 1953
 A;Title: The amino-acid sequence in the glycyl chain of insulin. 2. The investigation of peptides from enzymic hydrolysates.
 A;Reference number: A90342
 A;Accession: A90342
 A;Molecule type: protein
 A;Residues: 85-105 <SAN>
 R;Sanger, F.; Tuppy, H.
 Biochem. J. 49, 481-490, 1951
 A;Title: The amino-acid sequence in the phenylalanyl chain of insulin. 2. The investigation of peptides from enzymic hydrolysates.
 A;Reference number: A90341
 A;Accession: A90341
 A;Molecule type: protein
 A;Residues: 25-54 <SA2>
 R;Cheng, R.; Kawakishi, S.
 Eur. J. Biochem. 223, 759-764, 1994
 A;Title: Site-specific oxidation of histidine residues in glycated insulin mediated by Cu(2+).
 A;Reference number: S48184; MUID:94333378; PMID:8055951
 A;Accession: S48184
 A;Molecule type: protein
 A;Residues: 85-105 <CHE>
 A;Accession: S48185
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 25-30,'X',32-42,'X',44-54 <CH2>
 R;Ryle, A.P.; Sanger, F.; Smith, L.F.; Kitai, R.
 Biochem. J. 60, 541-556, 1955
 A;Title: The disulphide bonds of insulin.
 A;Reference number: A90343
 A;Contents: annotation; amides; disulfides
 R;Wenzel, T.; Eckerskorn, C.; Lottspeich, F.; Baumeister, W.
 FEBS Lett. 349, 205-209, 1994
 A;Title: Existence of a molecular ruler in proteasomes suggested by analysis of degradation products.
 A;Reference number: S46258; MUID:94326921; PMID:8050567
 A;Accession: S46258
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 25-54 <WEN>
 C;Superfamily: insulin

C;Keywords: hormone; pancreas
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-54/Domain: insulin chain B #status experimental <BCH>
F;25-54,85-105/Product: insulin #status experimental <MAT>
F;57-82/Domain: connecting peptide #status experimental <CPEP>
F;85-105/Domain: insulin chain A #status experimental <ACH>
F;31-91,43-104,90-95/Disulfide bonds: #status experimental

Query Match 79.2%; Score 366.5; DB 1; Length 105;
Best Local Similarity 80.2%; Pred. No. 1.7e-32;
Matches 69; Conservative 2; Mismatches 10; Indels 5; Gaps 1;

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Qy      1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60
          |||||
Db      25 FVNQHLCGSHLVEALYLVCGERGFFYTPKARREVEGPQVGALELAGGPGAG-----GLEG 79

Qy      61 SLQKRGIVEQCCTSICSLYQLENYCN 86
          |||||
Db      80 PPQKRGIVEQCCASVCSLYQLENYCN 105
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RESULT 15

INMS1

insulin 1 precursor - mouse

C;Species: Mus musculus (house mouse)

C;Date: 24-Apr-1984 #sequence_revision 14-Jul-1994 #text_change 09-Jul-2004

C;Accession: B26342; A48172; A01592; B61012

R;Wentworth, B.M.; Schaefer, I.M.; Villa-Komaroff, L.; Chirgwin, J.M.

J. Mol. Evol. 23, 305-312, 1986

A;Title: Characterization of the two nonallelic genes encoding mouse preproinsulin.

A;Reference number: A92965; MUID:87169768; PMID:3104603

A;Accession: B26342

A;Molecule type: DNA

A;Residues: 1-108 <WEN>

A;Cross-references: UNIPROT:P01325; GB:X04725; NID:g52712; PIDN:CAA28434.1;
PID:g52713

R;Sawa, T.; Ohgaku, S.; Morioka, H.; Yano, S.

J. Mol. Endocrinol. 5, 61-67, 1990

A;Title: Molecular cloning and DNA sequence analysis of preproinsulin genes in the NON mouse, an animal model of human non-obese, non-insulin-dependent diabetes mellitus.

A;Reference number: A48172; MUID:90372989; PMID:2397023

A;Accession: A48172

A;Status: not compared with conceptual translation

A;Molecule type: DNA

A;Residues: 1-108 <SAW>

R;Buenzli, H.F.; Glatthaar, B.; Kunz, P.; Muelhaupt, E.; Humbel, R.E.

Hoppe-Seyler's Z. Physiol. Chem. 353, 451-458, 1972

A;Title: Amino acid sequence of the two insulins from mouse (Mus musculus).

A;Reference number: A01592; MUID:72189455; PMID:5063718

A;Accession: A01592

A;Molecule type: protein

A;Residues: 25-54;88-108 <BUE>

R;Linde, S.; Nielsen, J.H.; Hansen, B.; Welinder, B.S.

J. Chromatogr. 462, 243-254, 1989

A;Title: Reversed-phase high-performance liquid chromatographic analyses of insulin biosynthesis in isolated rat and mouse islets.

A;Reference number: A61012; MUID:89292078; PMID:2661585

A;Accession: B61012

A;Molecule type: protein

A;Residues: 57-85 <LIN>

C;Superfamily: insulin

C;Keywords: hormone; pancreas

F;1-24/Domain: signal sequence #status predicted <SIG>

F;25-54/Domain: insulin chain B #status experimental <BCH>

F;25-54,88-108/Product: insulin #status experimental <MAT>

F;57-85/Domain: connecting peptide #status experimental <CPEP>

F;88-108/Domain: insulin chain A #status experimental <ACH>

F;31-94,43-107,93-98/Disulfide bonds: #status predicted

Query Match 79.0%; Score 366; DB 1; Length 108;

Best Local Similarity 81.4%; Pred. No. 2e-32;

Matches 70; Conservative 4; Mismatches 10; Indels 2; Gaps 1;

Qy 1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60

|| ||||| |||||||||||||||||||||:|||| || || |:|||| | | || |||||

Db 25 FVKQHLCGPHLVEALYLVCGERGFFYTPKSRREVEDPQVEQLELGGSP--GDLQTLALEV 82

Qy 61 SLQKRGIVEQCCTSICSLYQLENYCN 86

: |||||:|||||||||||||||||

Db 83 ARQKRGIVDQCCTSICSLYQLENYCN 108

Search completed: March 9, 2005, 04:20:10

Job time : 17.5018 secs

OM protein - protein search, using sw model

Run on: March 9, 2005, 01:51:08 ; Search time 75.5277 Seconds
 (without alignments)
 583.082 Million cell updates/sec

Title: US-10-054-873-4
 Perfect score: 463
 Sequence: 1 FVNQHLCGSHLVEALYLVCG.....IVEQCCTSICSLYQLENYCN 86

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : UniProt_03:*
 1: uniprot_sprot:*
 2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	463	100.0	110	1	INS_GORGO	Q6yk33 gorilla gor
2	463	100.0	110	1	INS_HUMAN	P01308 homo sapien
3	463	100.0	110	1	INS_PANTR	P30410 pan troglod
4	463	100.0	110	1	INS_PONPY	Q8hxx2 pongo pygma
5	456	98.5	110	1	INS_CERAE	P30407 cercopithec
6	456	98.5	110	1	INS_MACFA	P30406 macaca fasc
7	424	91.6	110	1	INS_RABIT	P01311 oryctolagus
8	417	90.1	110	1	INS_CANFA	P01321 canis famil
9	413	89.2	110	1	INS_SPETR	Q91xi3 spermophilu
10	394	85.1	86	1	INS_HORSE	P01310 equus cabal
11	394	85.1	110	1	INS2_MOUSE	P01326 mus musculu
12	394	85.1	110	1	INS2_RAT	P01323 rattus norv
13	392	84.7	108	1	INS_AOTTR	P67972 aotus trivi
14	392	84.7	110	1	INS_CRIL0	P01313 cricetulus
15	388	83.8	110	2	Q8WNW6	Q8wnw6 felis silve

16	385	83.2	110	1	INS1_RAT	P01322	rattus norv
17	383	82.7	108	1	INS_PIG	P01315	sus scrofa
18	377	81.4	110	1	INS_PSAOB	Q62587	psammomys o
19	366.5	79.2	105	1	INS_BOVIN	P01317	bos taurus
20	366	79.0	108	1	INS1_MOUSE	P01325	mus musculu
21	362.5	78.3	105	1	INS_SHEEP	P01318	ovis aries
22	342	73.9	65	2	Q8HZ80	Q8hz80	pongo pygma
23	342	73.9	65	2	Q8HZ81	Q8hz81	gorilla gor
24	334.5	72.2	108	1	INS_RODSP	P21563	rodentia sp
25	314	67.8	110	1	INS_CAVPO	P01329	cavia porce
26	277.5	59.9	109	1	INS_OCTDE	P17715	octodon deg
27	276.5	59.7	103	1	INS_SELRF	P51463	selasphorus
28	265.5	57.3	106	1	INS2_XENLA	P12707	xenopus lae
29	265.5	57.3	107	1	INS_CHICK	P67970	gallus gall
30	262.5	56.7	106	1	INS1_XENLA	P12706	xenopus lae
31	256.5	55.4	51	1	INS_BALPH	P67973	balaenopter
32	256.5	55.4	51	1	INS_ELEMA	P01316	elephas max
33	256.5	55.4	51	1	INS_PHYCA	P67974	physeter ca
34	256.5	55.4	81	1	INS_ANAPL	P01333	anas platyr
35	256	55.3	96	2	Q7M0U6	Q7m0u6	bacillus br
36	254.5	55.0	51	2	Q7M0G1	Q7m0g1	cricetidae
37	251.5	54.3	51	1	INS_ACOCA	P01324	acomys cahi
38	250.5	54.1	51	2	Q7M217	Q7m217	canavalia e
39	246.5	53.2	51	1	INS_BALBO	P01314	balaenopter
40	246.5	53.2	51	1	INS_CAMDR	P01320	camelus dro
41	246.5	53.2	51	1	INS_CAPHI	P01319	capra hircu
42	246.5	53.2	106	2	Q9I8Q7	Q9i8q7	rana pipien
43	245.5	53.0	51	1	INS_FELCA	P06306	felis silve
44	244.5	52.8	51	1	INS_SAISC	P67971	saimiri sci
45	239.5	51.7	51	1	INS_DIDMA	P18109	didelphis m

ALIGNMENTS

RESULT 1

INS_GORGO

ID INS_GORGO STANDARD; PRT; 110 AA.

AC Q6YK33;

DT 25-OCT-2004 (Rel. 45, Created)

DT 25-OCT-2004 (Rel. 45, Last sequence update)

DT 25-OCT-2004 (Rel. 45, Last annotation update)

DE Insulin precursor.

GN Name=INS;

OS Gorilla gorilla gorilla (Lowland gorilla).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.

OX NCBI_TaxID=9595;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=22833521; PubMed=12952878; DOI=10.1101/gr.948003;

RA Stead J.D.H., Hurles M.E., Jeffreys A.J.;

RT "Global haplotype diversity in the human insulin gene region.";

RL Genome Res. 13:2101-2111(2003).

CC -!- FUNCTION: Insulin decreases blood glucose concentration. It
 CC increases cell permeability to monosaccharides, amino acids and
 CC fatty acids. It accelerates glycolysis, the pentose phosphate

CC cycle, and glycogen synthesis in liver.
 CC -!- SUBUNIT: Heterodimer of a B chain and an A chain linked by two
 CC disulfide bonds.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the insulin family.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AY137500; AAN06935.1; -.
 DR InterPro; IPR004825; Ins/IGF/relax.
 DR InterPro; IPR003234; Mollusc_ins.
 DR Pfam; PF00049; Insulin; 1.
 DR PRINTS; PR00277; INSULINB.
 DR ProDom; PD015667; Mollusc_ins; 1.
 DR SMART; SM00078; ILGF; 1.
 DR PROSITE; PS00262; INSULIN; 1.
 KW Glucose metabolism; Hormone; Insulin family; Signal.
 FT SIGNAL 1 24 By similarity.
 FT CHAIN 25 54 Insulin B chain.
 FT PROPEP 57 87 C peptide.
 FT CHAIN 90 110 Insulin A chain.
 FT DISULFID 31 96 Interchain (By similarity).
 FT DISULFID 43 109 Interchain (By similarity).
 FT DISULFID 95 100 By similarity.
 SQ SEQUENCE 110 AA; 11981 MW; C2C3B23B85E520E5 CRC64;

Query Match 100.0%; Score 463; DB 1; Length 110;
 Best Local Similarity 100.0%; Pred. No. 8e-41;
 Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60
 |||
 Db 25 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 84
 Qy 61 SLQKRGIVEQCCTSICSLYQLENYCN 86
 |||
 Db 85 SLQKRGIVEQCCTSICSLYQLENYCN 110

RESULT 2

INS_HUMAN

ID INS_HUMAN STANDARD; PRT; 110 AA.
 AC P01308;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Insulin precursor.
 GN Name=INS;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=80120725; PubMed=6243748;
 RA Bell G.I., Pictet R.L., Rutter W.J., Cordell B., Tischer E.,
 RA Goodman H.M.;
 RT "Sequence of the human insulin gene.";
 RL Nature 284:26-32(1980).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=80236313; PubMed=6248962;
 RA Ullrich A., Dull T.J., Gray A., Brosius J., Sures I.;
 RT "Genetic variation in the human insulin gene.";
 RL Science 209:612-615(1980).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=80054779; PubMed=503234;
 RA Bell G.I., Swain W.F., Pictet R.L., Cordell B., Goodman H.M.,
 RA Rutter W.J.;
 RT "Nucleotide sequence of a cDNA clone encoding human preproinsulin.";
 RL Nature 282:525-527(1979).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=80147417; PubMed=6927840;
 RA Sures I., Goeddel D.V., Gray A., Ullrich A.;
 RT "Nucleotide sequence of human preproinsulin complementary DNA.";
 RL Science 208:57-59(1980).
 RN [5]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93364428; PubMed=8358440;
 RA Lucassen A.M., Bell J.I., Julier C., Lathrop M.;
 RT "Susceptibility to insulin dependent diabetes mellitus maps to a 4.1
 RT kb segment of DNA spanning the insulin gene and associated VNTR.";
 RL Nat. Genet. 4:305-310(1993).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Pancreas;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [7]
 RP SEQUENCE OF 1-59 FROM N.A.
 RC TISSUE=Blood;
 RA Fajardy I.I., Weill J.J., Stuckens C.C., Danze P.M.P.;
 RT "Description of a novel RFLP diallelic polymorphism (-127 BsgI C/G)
 RT within the 5' region of insulin gene.";
 RL Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
 RN [8]
 RP SEQUENCE OF 25-54 AND 90-110.
 RX PubMed=14426955;
 RA Nicol D.S.H.W., Smith L.F.;
 RT "Amino-acid sequence of human insulin.";
 RL Nature 187:483-485(1960).
 RN [9]
 RP SEQUENCE OF 57-87.
 RX MEDLINE=71116410; PubMed=5101771;
 RA Oyer P.E., Cho S., Peterson J.D., Steiner D.F.;
 RT "Studies on human proinsulin. Isolation and amino acid sequence of the
 RT human pancreatic C-peptide.";
 RL J. Biol. Chem. 246:1375-1386(1971).
 RN [10]
 RP SEQUENCE OF 57-87.
 RX MEDLINE=71257722; PubMed=5560404;
 RA Ko A., Smyth D.G., Markussen J., Sundby F.;
 RT "The amino acid sequence of the C-peptide of human proinsulin.";
 RL Eur. J. Biochem. 20:190-199(1971).
 RN [11]
 RP SYNTHESIS.
 RX MEDLINE=75077277; PubMed=4443293;
 RA Sieber P., Kamber B., Hartmann A., Joehl A., Riniker B., Rittel W.;
 RT "Total synthesis of human insulin under directed formation of the
 RT disulfide bonds.";
 RL Helv. Chim. Acta 57:2617-2621(1974).
 RN [12]
 RP SYNTHESIS OF 57-87.
 RX MEDLINE=75040007; PubMed=4803504;
 RA Naithani V.K.;
 RT "Studies on polypeptides, IV. The synthesis of C-peptide of human
 RT proinsulin.";
 RL Hoppe-Seyler's Z. Physiol. Chem. 354:659-672(1973).
 RN [13]
 RP SYNTHESIS OF 65-69 AND 70-73.
 RX MEDLINE=73161263; PubMed=4698555;
 RA Geiger R., Volk A.;
 RT "Synthesis of peptides with the properties of human proinsulin C
 RT peptides (hC peptide). 3. Synthesis of the sequences 14-17 and 9-13 of
 RT human proinsulin C peptides.";
 RL Chem. Ber. 106:199-205(1973).
 RN [14]
 RP SYNTHESIS OF 84-87.
 RX MEDLINE=73161261; PubMed=4698553;
 RA Geiger R., Jaeger G., Keonig W., Treuth G.;
 RT "Synthesis of peptides with the properties of human proinsulin C
 RT peptides (hC peptide). I. Scheme for the synthesis and preparation of
 RT the sequence 28-31 of human proinsulin C peptide.";
 RL Chem. Ber. 106:188-192(1973).

RN [15]
 RP VARIANT LOS ANGELES SER-48.
 RX MEDLINE=84016053; PubMed=6312455;
 RA Haneda M., Chan S.J., Kwok S.C.M., Rubenstein A.H., Steiner D.F.;
 RT "Studies on mutant human insulin genes: identification and sequence
 RT analysis of a gene encoding [SerB24]insulin."
 RL Proc. Natl. Acad. Sci. U.S.A. 80:6366-6370(1983).
 RN [16]
 RP VARIANTS LOS ANGELES SER-48 AND CHICAGO LEU-49.
 RX MEDLINE=84170233; PubMed=6424111;
 RA Shoelson S., Fickova M., Haneda M., Nahum A., Musso G., Kaiser E.T.,
 RA Rubenstein A.H., Tager H.;
 RT "Identification of a mutant human insulin predicted to contain a
 RT serine-for-phenylalanine substitution."
 RL Proc. Natl. Acad. Sci. U.S.A. 80:7390-7394(1983).
 RN [17]
 RP VARIANT PROVIDENCE ASP-34.
 RX MEDLINE=87175640; PubMed=3470784;
 RA Chan S.J., Seino S., Gruppuso P.A., Schwartz R., Steiner D.F.;
 RT "A mutation in the B chain coding region is associated with impaired
 RT proinsulin conversion in a family with hyperproinsulinemia."
 RL Proc. Natl. Acad. Sci. U.S.A. 84:2194-2197(1987).
 RN [18]
 RP VARIANT WAKAYAMA LEU-92.
 RX MEDLINE=87058122; PubMed=3537011;
 RA Sakura H., Iwamoto Y., Sakamoto Y., Kuzuya T., Hirata H.;
 RT "Structurally abnormal insulin in a diabetic patient. Characterization
 RT of the mutant insulin A3 (Val-->Leu) isolated from the pancreas."
 RL J. Clin. Invest. 78:1666-1672(1986).
 RN [19]
 RP VARIANT HIS-89.
 RX MEDLINE=90317021; PubMed=2196279;
 RA Barbetti F., Raben N., Kadowaki T., Cama A., Accili D., Gabbay K.H.,
 RA Merenich J.A., Taylor S.I., Roth J.;
 RT "Two unrelated patients with familial hyperproinsulinemia due to a
 RT mutation substituting histidine for arginine at position 65 in the
 RT proinsulin molecule: identification of the mutation by direct
 RT sequencing of genomic deoxyribonucleic acid amplified by polymerase
 RT chain reaction."
 RL J. Clin. Endocrinol. Metab. 71:164-169(1990).
 RN [20]
 RP VARIANT HIS-89.
 RX MEDLINE=85261996; PubMed=4019786;
 RA Shibasaki Y., Kawakami T., Kanazawa Y., Akanuma Y., Takaku F.;
 RT "Posttranslational cleavage of proinsulin is blocked by a point
 RT mutation in familial hyperproinsulinemia."
 RL J. Clin. Invest. 76:378-380(1985).
 RN [21]
 RP VARIANT KYOTO LEU-89.
 RX MEDLINE=92291307; PubMed=1601997;
 RA Yano H., Kitano N., Morimoto M., Polonsky K.S., Imura H., Seino Y.;
 RT "A novel point mutation in the human insulin gene giving rise to
 RT hyperproinsulinemia (proinsulin Kyoto)."
 RL J. Clin. Invest. 89:1902-1907(1992).
 RN [22]
 RP STRUCTURE BY NMR.
 RX MEDLINE=91104966; PubMed=2271664;

RA Hua Q.-X., Weiss M.A.;
 RT "Toward the solution structure of human insulin: sequential 2D 1H NMR
 RT assignment of a des-pentapeptide analogue and comparison with crystal
 RT structure.";
 RL Biochemistry 29:10545-10555(1990).
 RN [23]
 RP STRUCTURE BY NMR.
 RX MEDLINE=91242467; PubMed=2036420;
 RA Hua Q.-X., Weiss M.A.;
 RT "Comparative 2D NMR studies of human insulin and des-pentapeptide
 RT insulin: sequential resonance assignment and implications for protein
 RT dynamics and receptor recognition.";
 RL Biochemistry 30:5505-5515(1991).
 RN [24]
 RP STRUCTURE BY NMR.
 RX MEDLINE=91265527; PubMed=1646635; DOI=10.1016/0167-4838(91)90098-K;
 RA Hua Q.-X., Weiss M.A.;
 RT "Two-dimensional NMR studies of Des-(B26-B30)-insulin: sequence-
 RT specific resonance assignments and effects of solvent composition.";

Query Match 100.0%; Score 463; DB 1; Length 110;
 Best Local Similarity 100.0%; Pred. No. 8e-41;
 Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60
 ||||||||||||||||||
 Db 25 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 84

 Qy 61 SLQKRGIVEQCCTSICSLYQLENYCN 86
 ||||||||||||||
 Db 85 SLQKRGIVEQCCTSICSLYQLENYCN 110

RESULT 3

INS_PANTR

ID INS_PANTR STANDARD; PRT; 110 AA.
 AC P30410;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Insulin precursor.
 GN Name=INS;
 OS Pan troglodytes (Chimpanzee).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
 OX NCBI_TaxID=9598;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92219953; PubMed=1560757;
 RA Seino S., Bell G.I., Li W.;
 RT "Sequences of primate insulin genes support the hypothesis of a slower
 RT rate of molecular evolution in humans and apes than in monkeys.";
 RL Mol. Biol. Evol. 9:193-203(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22833521; PubMed=12952878; DOI=10.1101/gr.948003;
 RA Stead J.D.H., Hurles M.E., Jeffreys A.J.;

RT "Global haplotype diversity in the human insulin gene region.";
 RL Genome Res. 13:2101-2111(2003).
 CC -!- FUNCTION: Insulin decreases blood glucose concentration. It
 CC increases cell permeability to monosaccharides, amino acids and
 CC fatty acids. It accelerates glycolysis, the pentose phosphate
 CC cycle, and glycogen synthesis in liver.
 CC -!- SUBUNIT: Heterodimer of a B chain and an A chain linked by two
 CC disulfide bonds.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the insulin family.
 CC -----
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 CC -----
 DR EMBL; X61089; CAA43403.1; -.
 DR EMBL; AY137497; AAN06933.1; -.
 DR PIR; A42179; A42179.
 DR HSSP; P01308; 1AI0.
 DR InterPro; IPR004825; Ins/IGF/relax.
 DR Pfam; PF00049; Insulin; 1.
 DR PRINTS; PR00277; INSULINB.
 DR ProDom; PD015667; Mollusc_ins; 1.
 DR PROSITE; PS00262; INSULIN; 1.
 KW Glucose metabolism; Hormone; Insulin family; Signal.
 FT SIGNAL 1 24 By similarity.
 FT CHAIN 25 54 Insulin B chain.
 FT PROPEP 57 87 C peptide.
 FT CHAIN 90 110 Insulin A chain.
 FT DISULFID 31 96 Interchain (By similarity).
 FT DISULFID 43 109 Interchain (By similarity).
 FT DISULFID 95 100 By similarity.
 SQ SEQUENCE 110 AA; 12025 MW; 41EB8DF79837CEF5 CRC64;

Query Match 100.0%; Score 463; DB 1; Length 110;
 Best Local Similarity 100.0%; Pred. No. 8e-41;
 Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 25 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 84
 QY 61 SLQKRGIVEQCCTSICSLYQLENYCN 86
 ||||||||||||||||||||
 Db 85 SLQKRGIVEQCCTSICSLYQLENYCN 110

RESULT 4
 INS_PONPY
 ID INS_PONPY STANDARD; PRT; 110 AA.
 AC Q8HXV2;
 DT 05-JUL-2004 (Rel. 44, Created)
 DT 05-JUL-2004 (Rel. 44, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Insulin precursor.
 GN Name=INS;
 OS Pongo pygmaeus (Orangutan).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
 OX NCBI_TaxID=9600;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22833521; PubMed=12952878; DOI=10.1101/gr.948003;
 RA Stead J.D.H., Hurles M.E., Jeffreys A.J.;
 RT "Global haplotype diversity in the human insulin gene region.";
 RL Genome Res. 13:2101-2111(2003).
 CC -!- FUNCTION: Insulin decreases blood glucose concentration. It
 CC increases cell permeability to monosaccharides, amino acids and
 CC fatty acids. It accelerates glycolysis, the pentose phosphate
 CC cycle, and glycogen synthesis in liver.
 CC -!- SUBUNIT: Heterodimer of a B chain and an A chain linked by two
 CC disulfide bonds.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the insulin family.
 CC -----
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 CC -----
 DR EMBL; AY137503; AAN06937.1; -.
 DR HSSP; P01308; 1AI0.
 DR InterPro; IPR004825; Ins/IGF/relax.
 DR Pfam; PF00049; Insulin; 1.
 DR PRINTS; PR00277; INSULINB.
 DR ProDom; PD015667; Mollusc_ins; 1.
 DR SMART; SM00078; IIGF; 1.
 DR PROSITE; PS00262; INSULIN; 1.
 KW Glucose metabolism; Hormone; Insulin family; Signal.
 FT SIGNAL 1 24 By similarity.
 FT CHAIN 25 54 Insulin B chain.
 FT PROPEP 57 87 C peptide.
 FT CHAIN 90 110 Insulin A chain.
 FT DISULFID 31 96 Interchain (By similarity).
 FT DISULFID 43 109 Interchain (By similarity).
 FT DISULFID 95 100 By similarity.
 SQ SEQUENCE 110 AA; 12038 MW; 22D2B32B94F520F8 CRC64;

Query Match 100.0%; Score 463; DB 1; Length 110;
 Best Local Similarity 100.0%; Pred. No. 8e-41;
 Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 25 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 84
 Qy 61 SLQKRGIVEQCCTSICSLYQLENYCN 86

RESULT 5

INS_CERAE

ID INS_CERAE STANDARD; PRT; 110 AA.
AC P30407; P01309;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Insulin precursor.
GN Name=INS;
OS Cercopithecus aethiops (Green monkey) (Grivet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=9534;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92219953; PubMed=1560757;
RA Seino S., Bell G.I., Li W.;
RT "Sequences of primate insulin genes support the hypothesis of a slower
RT rate of molecular evolution in humans and apes than in monkeys.";
RL Mol. Biol. Evol. 9:193-203(1992).
RN [2]
RP SEQUENCE OF 57-87.
RX MEDLINE=72258016; PubMed=4626369;
RA Peterson J.D., Nehrlich S., Oyer P.E., Steiner D.F.;
RT "Determination of the amino acid sequence of the monkey, sheep, and
RT dog proinsulin C-peptides by a semi-micro Edman degradation
RT procedure.";
RL J. Biol. Chem. 247:4866-4871(1972).
CC -!- FUNCTION: Insulin decreases blood glucose concentration. It
CC increases cell permeability to monosaccharides, amino acids and
CC fatty acids. It accelerates glycolysis, the pentose phosphate
CC cycle, and glycogen synthesis in liver.
CC -!- SUBUNIT: Heterodimer of a B chain and an A chain linked by two
CC disulfide bonds.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the insulin family.
CC -----
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CC -----
DR EMBL; X61092; CAA43405.1; -.
DR PIR; B42179; B42179.
DR HSSP; P01308; 1AI0.
DR InterPro; IPR004825; Ins/IGF/relax.
DR Pfam; PF00049; Insulin; 1.
DR PRINTS; PR00277; INSULINB.
DR ProDom; PD015667; Mollusc_ins; 1.

DR SMART; SM00078; IIGF; 1.
 DR PROSITE; PS00262; INSULIN; 1.
 KW Direct protein sequencing; Glucose metabolism; Hormone;
 KW Insulin family; Signal.
 FT SIGNAL 1 24
 FT CHAIN 25 54 Insulin B chain.
 FT PROPEP 57 87 C peptide.
 FT CHAIN 90 110 Insulin A chain.
 FT DISULFID 31 96 Interchain.
 FT DISULFID 43 109 Interchain.
 FT DISULFID 95 100
 SQ SEQUENCE 110 AA; 12019 MW; 95AlF54BE7B247F9 CRC64;

Query Match 98.5%; Score 456; DB 1; Length 110;
 Best Local Similarity 98.8%; Pred. No. 4.3e-40;
 Matches 85; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60
 |||
 Db 25 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDPQVGQVELGGGPGAGSLQPLALEG 84
 Qy 61 SLQKRGIVEQCCTSICSLYQLENYCN 86
 |||
 Db 85 SLQKRGIVEQCCTSICSLYQLENYCN 110

RESULT 6

INS_MACFA

ID INS_MACFA STANDARD; PRT; 110 AA.
 AC P30406; P01309;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Insulin precursor.
 GN Name=INS;
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
 OC Cercopithecinae; Macaca.
 OX NCBI_TaxID=9541;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=83080474; PubMed=6184262; DOI=10.1016/0378-1119(82)90004-X;
 RA Wetekam W., Groneberg J., Leineweber M., Wengenmayer F.,
 RA Winnacker E.-L.;
 RT "The nucleotide sequence of cDNA coding for preproinsulin from the
 RT primate Macaca fascicularis."
 RL Gene 19:179-183(1982).
 CC -!- FUNCTION: Insulin decreases blood glucose concentration. It
 CC increases cell permeability to monosaccharides, amino acids and
 CC fatty acids. It accelerates glycolysis, the pentose phosphate
 CC cycle, and glycogen synthesis in liver.
 CC -!- SUBUNIT: Heterodimer of a B chain and an A chain linked by two
 CC disulfide bonds.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the insulin family.
 CC -----

RA Devaskar S.U., Giddings S.J., Rajakumar P.A., Carnaghi L.R.,
 RA Menon R.K., Zahm D.S.;
 RT "Insulin gene expression and insulin synthesis in mammalian neuronal
 RT cells.";
 RL J. Biol. Chem. 269:8445-8454(1994).
 RN [2]
 RP SEQUENCE OF 25-54 AND 90-110.
 RX MEDLINE=66160119; PubMed=5949593; DOI=10.1016/0002-9343(66)90145-8;
 RA Smith L.F.;
 RT "Species variation in the amino acid sequence of insulin.";
 RL Am. J. Med. 40:662-666(1966).
 RN [3]
 RP SEQUENCE OF 56-110 FROM N.A.
 RA Giddings S.J., Carnaghi L.R., Devaskar S.U.;
 RL Submitted (APR-1991) to the EMBL/GenBank/DDBJ databases.
 CC -!- FUNCTION: Insulin decreases blood glucose concentration. It
 CC increases cell permeability to monosaccharides, amino acids and
 CC fatty acids. It accelerates glycolysis, the pentose phosphate
 CC cycle, and glycogen synthesis in liver.
 CC -!- SUBUNIT: Heterodimer of a B chain and an A chain linked by two
 CC disulfide bonds.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the insulin family.
 CC -----
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 CC -----
 DR EMBL; U03610; AAA19033.1; -.
 DR EMBL; M61153; AAA17540.1; -.
 DR PIR; A53438; INRB.
 DR HSSP; P01308; 1EV6.
 DR InterPro; IPR004825; Ins/IGF/relax.
 DR Pfam; PF00049; Insulin; 1.
 DR PRINTS; PR00277; INSULINB.
 DR ProDom; PD015667; Mollusc_ins; 1.
 DR SMART; SM00078; IIGF; 1.
 DR PROSITE; PS00262; INSULIN; 1.
 KW Direct protein sequencing; Glucose metabolism; Hormone;
 KW Insulin family; Signal.
 FT SIGNAL 1 24
 FT CHAIN 25 54 Insulin B chain.
 FT PROPEP 57 87 C peptide.
 FT CHAIN 90 110 Insulin A chain.
 FT DISULFID 31 96 Interchain.
 FT DISULFID 43 109 Interchain.
 FT DISULFID 95 100
 FT CONFLICT 83 83 E -> Y (in Ref. 3).
 SQ SEQUENCE 110 AA; 11838 MW; 82D2975B85D77FA8 CRC64;

 Query Match 91.6%; Score 424; DB 1; Length 110;
 Best Local Similarity 90.7%; Pred. No. 1e-36;
 Matches 78; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60
 |||||:|||||
 Db 25 FVNQHLCGSHLVEALYLVCGERGFFYTPKSRREVEELQVGQAEELGGGPGAGGLQPSALEL 84
 Qy 61 SLQKRGIVEQCCTSICSLYQLENYCN 86
 :|||||
 Db 85 ALQKRGIVEQCCTSICSLYQLENYCN 110

RESULT 8

INS_CANFA

ID INS_CANFA STANDARD; PRT; 110 AA.
 AC P01321;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Insulin precursor.
 GN Name=INS;
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=83109071; PubMed=6296142;
 RA Kwok S.C.M., Chan S.J., Steiner D.F.;
 RT "Cloning and nucleotide sequence analysis of the dog insulin gene.
 RT Coded amino acid sequence of canine preproinsulin predicts an
 RT additional C-peptide fragment.";
 RL J. Biol. Chem. 258:2357-2363(1983).
 RN [2]
 RP SEQUENCE OF 25-54 AND 90-110.
 RX MEDLINE=66160119; PubMed=5949593; DOI=10.1016/0002-9343(66)90145-8;
 RA Smith L.F.;
 RT "Species variation in the amino acid sequence of insulin.";
 RL Am. J. Med. 40:662-666(1966).
 CC -!- FUNCTION: Insulin decreases blood glucose concentration. It
 CC increases cell permeability to monosaccharides, amino acids and
 CC fatty acids. It accelerates glycolysis, the pentose phosphate
 CC cycle, and glycogen synthesis in liver.
 CC -!- SUBUNIT: Heterodimer of a B chain and an A chain linked by two
 CC disulfide bonds.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the insulin family.
 CC -----
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 CC -----
 DR EMBL; V00179; CAA23475.1; -.
 DR PIR; A92413; IPDG.
 DR HSSP; P01317; 1APH.

DR InterPro; IPR004825; Ins/IGF/relax.
 DR Pfam; PF00049; Insulin; 1.
 DR PRINTS; PR00277; INSULINB.
 DR ProDom; PD015667; Mollusc_ins; 1.
 DR SMART; SM00078; IIGF; 1.
 DR PROSITE; PS00262; INSULIN; 1.
 KW Direct protein sequencing; Glucose metabolism; Hormone;
 KW Insulin family; Signal.
 FT SIGNAL 1 24
 FT CHAIN 25 54 Insulin B chain.
 FT PROPEP 57 87 C peptide.
 FT CHAIN 90 110 Insulin A chain.
 FT DISULFID 31 96 Interchain.
 FT DISULFID 43 109 Interchain.
 FT DISULFID 95 100
 SQ SEQUENCE 110 AA; 12190 MW; A574791864A4FB98 CRC64;

Query Match 90.1%; Score 417; DB 1; Length 110;
 Best Local Similarity 89.5%; Pred. No. 5.4e-36;
 Matches 77; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

Qy 1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60
 |||||
 Db 25 FVNQHLCGSHLVEALYLVCGERGFFYTPKARREVEDLQVRDVELAGAPGEGGLQPLALEG 84
 Qy 61 SLQKRGIVEQCCTSICSLYQLENYCN 86
 :|||
 Db 85 ALQKRGIVEQCCTSICSLYQLENYCN 110

RESULT 9

INS_SPETR
 ID INS_SPETR STANDARD; PRT; 110 AA.
 AC Q91XI3;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Insulin precursor.
 GN Name=INS;
 OS *Spermophilus tridecemlineatus* (Thirteen-lined ground squirrel).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
 OC *Spermophilus*.
 OX NCBI_TaxID=43179;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Pancreas;
 RA Tredrea M.M., Buck M.J., Guhaniyogi J., Squire T.L., Andrews M.T.;
 RT "Regulation of PDK4 expression in a hibernating mammal."
 RL Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
 CC -!- FUNCTION: Insulin decreases blood glucose concentration. It
 CC increases cell permeability to monosaccharides, amino acids and
 CC fatty acids. It accelerates glycolysis, the pentose phosphate
 CC cycle, and glycogen synthesis in liver.
 CC -!- SUBUNIT: Heterodimer of a B chain and an A chain linked by two
 CC disulfide bonds.
 CC -!- SUBCELLULAR LOCATION: Secreted.

```

CC  -- SIMILARITY: Belongs to the insulin family.
CC  -----
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CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL; AY038604; AAK72558.1; -.
DR  HSSP; P01308; 1EV6.
DR  InterPro; IPR004825; Ins/IGF/relax.
DR  Pfam; PF00049; Insulin; 1.
DR  PRINTS; PR00277; INSULINB.
DR  ProDom; PD015667; Mollusc_ins; 1.
DR  SMART; SM00078; IIGF; 1.
DR  PROSITE; PS00262; INSULIN; 1.
KW  Glucose metabolism; Hormone; Insulin family; Signal.
FT  SIGNAL          1      24      By similarity.
FT  CHAIN           25     54      Insulin B chain.
FT  PROPEP          57     87      C peptide.
FT  CHAIN           90    110      Insulin A chain.
FT  DISULFID        31     96      Interchain (By similarity).
FT  DISULFID        43    109      Interchain (By similarity).
FT  DISULFID        95    100      By similarity.
SQ  SEQUENCE      110 AA;  12004 MW;  4511768D6622BEE5 CRC64;

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Query Match          89.2%;  Score 413;  DB 1;  Length 110;
Best Local Similarity 89.5%;  Pred. No. 1.4e-35;
Matches 77;  Conservative 3;  Mismatches 6;  Indels 0;  Gaps 0;

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Qy      1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60
        |||||:|||||:|
Db      25 FVNQHLCGSHLVEALYLVCGERGFFYTPKSRREVVEEQGGQVELGGGPGAGLPQPLALEM 84

Qy      61 SLQKRGIVEQCCTSICSLYQLENYCN 86
        :|||||
Db      85 ALQKRGIVEQCCTSICSLYQLENYCN 110

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RESULT 10

INS_HORSE

```

ID  INS_HORSE      STANDARD;      PRT;      86 AA.
AC  P01310;
DT  21-JUL-1986 (Rel. 01, Created)
DT  21-JUL-1986 (Rel. 01, Last sequence update)
DT  25-OCT-2004 (Rel. 45, Last annotation update)
DE  Insulin precursor.
GN  Name=INS;
OS  Equus caballus (Horse).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX  NCBI_TaxID=9796;
RN  [1]
RP  SEQUENCE OF 1-30 AND 66-86.
RX  PubMed=13373434;

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DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Insulin 2 precursor.
 GN Name=Ins2; Synonyms=Ins-2;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87169768; PubMed=3104603;
 RA Wentworth B.M., Schaefer I.M., Villa-Komaroff L., Chirgwin J.M.;
 RT "Characterization of the two nonallelic genes encoding mouse
 RT preproinsulin.";
 RL J. Mol. Evol. 23:305-312(1986).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NON;
 RX MEDLINE=90372989; PubMed=2397023;
 RA Sawa T., Ohgaku S., Morioka H., Yano S.;
 RT "Molecular cloning and DNA sequence analysis of preproinsulin genes in
 RT the NON mouse, an animal model of human non-obese, non-insulin-
 RT dependent diabetes mellitus.";
 RL J. Mol. Endocrinol. 5:61-67(1990).
 RN [3]
 RP SEQUENCE OF 25-54 AND 90-110.
 RX MEDLINE=72189455; PubMed=5063718;
 RA Buenzli H.F., Glatthaar B., Kunz P., Muelhaupt E., Humbel R.E.;
 RT "Amino acid sequence of the two insulins from mouse (Maus musculus).";
 RL Hoppe-Seyler's Z. Physiol. Chem. 353:451-458(1972).
 CC -!- FUNCTION: Insulin decreases blood glucose concentration. It
 CC increases cell permeability to monosaccharides, amino acids and
 CC fatty acids. It accelerates glycolysis, the pentose phosphate
 CC cycle, and glycogen synthesis in liver.
 CC -!- SUBUNIT: Heterodimer of a B chain and an A chain linked by two
 CC disulfide bonds.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the insulin family.
 CC -----
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 CC -----
 DR EMBL; X04724; CAA28433.1; -.
 DR PIR; A26342; INMS2.
 DR HSSP; P01317; 1APH.
 DR MGD; MGI:96573; Ins2.
 DR GO; GO:0005634; C:nucleus; IDA.
 DR GO; GO:0005732; C:small nucleolar ribonucleoprotein complex; IDA.
 DR GO; GO:0000187; P:activation of MAPK; IDA.
 DR GO; GO:0006006; P:glucose metabolism; IMP.
 DR GO; GO:0008286; P:insulin receptor signaling pathway; IDA.
 DR GO; GO:0016042; P:lipid catabolism; IDA.
 DR GO; GO:0042981; P:regulation of apoptosis; IMP.

DR GO; GO:0042325; P:regulation of phosphorylation; IDA.
 DR GO; GO:0006983; P:response to ER-overload; IMP.
 DR InterPro; IPR004825; Ins/IGF/relax.
 DR Pfam; PF00049; Insulin; 1.
 DR PRINTS; PR00277; INSULINB.
 DR ProDom; PD015667; Mollusc_ins; 1.
 DR SMART; SM00078; ILGF; 1.
 DR PROSITE; PS00262; INSULIN; 1.
 KW Direct protein sequencing; Glucose metabolism; Hormone;
 KW Insulin family; Multigene family; Signal.
 FT SIGNAL 1 24
 FT CHAIN 25 54 Insulin 2 B chain.
 FT PROPEP 57 87 C peptide.
 FT CHAIN 90 110 Insulin 2 A chain.
 FT DISULFID 31 96 Interchain.
 FT DISULFID 43 109 Interchain.
 FT DISULFID 95 100
 SQ SEQUENCE 110 AA; 12364 MW; 3554C8803D24FDAD CRC64;

Query Match 85.1%; Score 394; DB 1; Length 110;
 Best Local Similarity 84.9%; Pred. No. 1.4e-33;
 Matches 73; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

Qy 1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60
 || ||||| :||| || || :||| || || || ||
 Db 25 FVKQHLCGSHLVEALYLVCGERGFFYTPMSRREVEDPQVAQLELGGGPGAGDLQTLALEV 84
 Qy 61 SLQKRGIVEQCCTSICSLYQLENYCN 86
 : ||||| :||| ||||| |||||
 Db 85 AQQKRGIVDQCCTSICSLYQLENYCN 110

RESULT 12

INS2_RAT
 ID INS2_RAT STANDARD; PRT; 110 AA.
 AC P01323;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Insulin 2 precursor.
 GN Name=Ins2; Synonyms=Ins-2;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Liver;
 RX MEDLINE=80045035; PubMed=498284; DOI=10.1016/0092-8674(79)90071-0;
 RA Lomedico P., Rosenthal N., Efstratiadis A., Gilbert W., Kolodner R.,
 RA Tizard R.;
 RT "The structure and evolution of the two nonallelic rat preproinsulin
 RT genes."
 RL Cell 18:545-558(1979).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86310882; PubMed=2427930;

RA Soares M.B., Schin E., Henderson A., Karathanasis S.K., Cate R.,
 RA Zeitlin S., Chirgwin J., Efstratiadis A.;
 RT "RNA-mediated gene duplication: the rat preproinsulin I gene is a
 RT functional retroposon.";
 RL Mol. Cell. Biol. 5:2090-2103(1985).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=80240379; PubMed=6249167;
 RA Lomedico P.T., Rosenthal N., Kolodner R., Efstratiadis A., Gilbert W.;
 RT "The structure of rat preproinsulin genes.";
 RL Ann. N. Y. Acad. Sci. 343:425-432(1980).
 RN [4]
 RP SEQUENCE OF 25-54 AND 90-110.
 RX MEDLINE=70067613; PubMed=4311938;
 RA Steiner D.F., Clark J.L., Nolan C., Rubenstein A.H., Margoliash E.,
 RA Aten B., Oyer P.E.;
 RT "Proinsulin and the biosynthesis of insulin.";
 RL Recent Prog. Horm. Res. 25:207-282(1969).
 RN [5]
 RP SEQUENCE OF 57-87.
 RX MEDLINE=73061498; PubMed=4640931;
 RA Tager H.S., Steiner D.F.;
 RT "Primary structures of the proinsulin connecting peptides of the rat
 RT and the horse.";
 RL J. Biol. Chem. 247:7936-7940(1972).
 RN [6]
 RP SEQUENCE OF 57-87, AND REVISIONS.
 RX MEDLINE=72177385; PubMed=4554104;
 RA Markussen J., Sundby F.;
 RT "Rat-proinsulin C-peptides. Amino-acid sequences.";
 RL Eur. J. Biochem. 25:153-162(1972).
 CC -!- FUNCTION: Insulin decreases blood glucose concentration. It
 CC increases cell permeability to monosaccharides, amino acids and
 CC fatty acids. It accelerates glycolysis, the pentose phosphate
 CC cycle, and glycogen synthesis in liver.
 CC -!- SUBUNIT: Heterodimer of a B chain and an A chain linked by two
 CC disulfide bonds.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the insulin family.
 CC -----
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 CC -----
 DR EMBL; V01243; CAA24560.1; -.
 DR EMBL; J00748; AAA41443.1; -.
 DR EMBL; M25585; AAA41440.1; -.
 DR EMBL; M25583; AAA41440.1; JOINED.
 DR PIR; B90789; IPRT2.
 DR HSSP; P01317; IAPH.
 DR RGD; 2916; Ins2.
 DR InterPro; IPR004825; Ins/IGF/relax.
 DR Pfam; PF00049; Insulin; 1.


```

DR PRINTS; PR00277; INSULINB.
DR ProDom; PD015667; Mollusc_ins; 1.
DR SMART; SM00078; IIGF; 1.
DR PROSITE; PS00262; INSULIN; 1.
KW Direct protein sequencing; Glucose metabolism; Hormone;
KW Insulin family; Multigene family; Signal.
FT SIGNAL 1 24
FT CHAIN 25 54 Insulin 2 B chain.
FT PROPEP 57 87 C peptide.
FT CHAIN 90 110 Insulin 2 A chain.
FT DISULFID 31 96 Interchain.
FT DISULFID 43 109 Interchain.
FT DISULFID 95 100
SQ SEQUENCE 110 AA; 12339 MW; 3A626DA98C86F3CA CRC64;

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RESULT 13

08WNW.6

Query Match 83.8%; Score 388; DB 2; Length 110;
Best Local Similarity 83.7%; Pred. No. 6.1e-33;
Matches 72; Conservative 2; Mismatches 12; Indels 0; Gaps 0;

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Qy      1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60
          |||||
Db      25 FVNQHLCGSHLVEALYLVCGERGFFYTPKARREAEDLQGKDAELGEAPGAGGLQPSALEA 84
          |||||
Qy      61 SLQKRGIVEQCCTSICSLYQLENYCN 86
          |||||
Db      85 PLOKRGIVEOCCASVCSLYOLEHYCN 110
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Search completed: March 9, 2005, 04:18:15
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